!!° #Need by #
9/29/03

SEARCH REQUEST FORM
Scientific and Technical Information Center

9/23 unp
Access DB# 104293
9/22 20

Requester's Full Name: BENNETT CYUSA   Examiner # : 73815   Date: 9/23/03
Art Unit: 1639   Phone Number 305-7556   Serial Number: 09/848,798
(Mail Box) and Bldg/Room Location: CM1   Results Format Preferred (circle): PAPER (DISK) E-MAIL
3B01

If more than one search is submitted, please prioritize searches in order of need.
****

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Rh(D) binding proteins —

Inventors (please provide full names): DONALD L. Siegel

Earliest Priority Filing Date: 6/67/97

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please senach

1) SEQ Id 97-393 (cDNA)   NA

2) SEQ Id 28-131 (protein: anti-RH(D) chain   AA
                                              E03)

IN
All relevant databases
— provide at least 20 hits which
"comprise" these sequences.

thanks
Ex celsr1
                                         , elected
                                          11-13
See attached BIB + claims (22-37)

****

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OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: September 24, 2003, 04:42:55 ; Search time 71 seconds
(without alignments)
292.862 Million cell updates/sec

Title: US-09-848-798A-28
Perfect score: 689
Sequence: 1 EVQLLESGVESGGGLVKPGG...........WVRSDGMDVWGQGTTVIVSS 131

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*
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23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	689	100.0	131	22	AAG93585	Human anti-Rh(D) c
2	643	93.3	127	22	AAG93584	Human anti-Rh(D) c
3	511.5	74.2	256	23	ABP43307	Human BLyS binding
4	509	73.9	248	23	ABP44902	Human BLyS binding
5	507.5	73.7	245	20	AAY06717	Antibody 12B5 sing
6	506.5	73.5	247	23	ABP45753	Human BLyS binding
7	504.5	73.2	116	23	AAE28870	Human KDR (VEGFR-2
8	504.5	73.2	116	24	ABJ26763	VEGF binding relat
9	499.5	72.5	116	23	AAE28873	Human KDR (VEGFR-2

ALIGNMENTS

RESULT 1
AAG93585
ID   AAG93585 standard; Protein; 131 AA.
XX
AC   AAG93585;
XX
DT   14-SEP-2001 (first entry)
XX
DE   Human anti-Rh(D) chain E03 protein sequence.
KW   Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW   red blood cell; Rh phenotype; diagnosis; therapeutic.
OS   Homo sapiens.
XX
PN   US6255455-B1.
XX
PD   03-JUL-2001.
XX
PF   29-JAN-1999; 99US-0240274.
XX
PR   11-OCT-1996; 96US-0028550.
PR   10-APR-1998; 98US-0081380.
PR   27-JUN-1997; 97US-0884045.
XX
PA   (UYPE-) UNIV PENNSYLVANIA.
XX
PI   Siegel DL;
XX
DR   WPI; 2001-388931/41.
DR   N-PSDB; AAH68642.-

10	499.5	72.5	116	24	ABJ26766	VEGF binding relat
11	499.5	72.5	249	23	ABP45845	Human BLyS binding
12	499	72.4	125	23	ABG77142	Anti-IGF-1R antibo
13	498	72.3	241	23	ABP45926	Human BLyS binding
14	497.5	72.2	247	23	ABP45692	Human BLyS binding
15	496.5	72.1	473	23	ABG77162	Germline protein s
16	496.5	72.1	152	22	AAB99111	Germline protein S
17	495.5	71.9	249	23	ABP44963	Human BLyS binding
18	495.5	71.9	248	23	ABP45963	Human BLyS binding
19	494.5	71.8	262	23	ABP46070	Human BLyS binding
20	492.5	71.6	252	23	ABP45623	Human BLyS binding
21	491.5	71.3	128	22	AAE07014	Human heavy chain
22	491	71.3	250	23	ABP45168	Human BLyS binding
23	491	71.3	255	23	ABP45597	Human BLyS binding
24	490.5	71.2	124	23	AAO18439	Anti-GD2 antibody
25	489.5	71.0	248	23	ABP45954	Human BLyS binding
26	489	71.0	244	23	ABP45980	Human BLyS binding
27	488.5	70.9	125	22	AAB62746	Human HIV-1 monocl
28	488.5	70.8	256	23	ABP45198	Human BLyS binding
29	487.5	70.8	258	23	ABP45830	Human BLyS binding
30	486	70.5	121	24	ABP56504	Human anti-Fc-epsi
31	486	70.5	121	24	ABP56506	Human anti-Fc-epsi
32	485.5	70.5	250	23	ABP45602	Human BLyS binding
33	485	70.4	127	22	AAE07024	Human heavy chain
34	485	70.4	173	20	AAY34306	Human heavy chain
35	484	70.2	255	23	ABP45808	Human BLyS binding
36	484	70.2	470	23	ABG77158	Germline protein s
37	483	70.1	121	23	AAE07029	Human heavy chain
38	483	70.1	121	24	ABP56507	Human anti-Fc-epsi
39	483	70.1	125	22	AAE07013	Human heavy chain
40	483	70.1	127	22	AAU02616	Anti-adipocyte mon
41	483	70.1	556	20	AAW90218	Bispecific tetrava
42	482.5	70.0	124	23	AAW90285	Human anti-GPIIb/I
43	482.5	70.0	252	23	ABP45351	Human BLyS binding
44	482.5	70.0	253	24	ABJ19830	Human VEGF-2 relat
45	481	69.8	123	18	AAW08582	Human antibody C4.

```
PT   New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT   diagnostics requiring a human instead of an animal antibody and in
PT   therapeutic medicine -
XX
PS   Claim 1; Column 43; 162pp; English.
XX
CC   The present invention describes an isolated Rh(D) binding protein,
CC   preferably a human antibody, (I) having an amino acid sequence comprising
CC   one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC   immunostimulant activity, and can be used as an immune system stimulant.
CC   (I) can be used in diagnostics and therapeutic medicine. The antibodies
CC   are used in diagnostics that require human antibodies instead of animal
CC   antibodies, such as determine the Rh phenotype of human red blood cells.
CC   AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC   AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC   chain CDR3 amino acid sequences which are given in the exemplification
CC   of the present invention.
XX
SQ   Sequence   131 AA;

Query Match             100.0%;  Score 689;  DB 22;  Length 131;
Best Local Similarity   100.0%;  Pred. No. 9.1e-55;
Matches 131;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1  EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT  60
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Db    1  EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT  60

Qy   61  YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120

Qy  121  WGQGTTVIVSS 131
         |||||||||||
Db  121  WGQGTTVIVSS 131


RESULT 2
AAG93584
ID   AAG93584 standard; Protein; 127 AA.
XX
AC   AAG93584;
XX
DT   14-SEP-2001 (first entry)
XX
DE   Human anti-Rh(D) chain E01is protein sequence.
XX
KW   Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW   red blood cell; Rh phenotype; diagnosis; therapeutic.
XX
OS   Homo sapiens.
XX
PN   US625455-B1.
XX
PD   03-JUL-2001.
XX
PF   29-JAN-1999;  99US-0240274.
XX
PR   11-OCT-1996;  96US-0028550.
PR   10-APR-1998;  98US-0081380.
PR   27-JUN-1997;  97US-0884045.
XX
PA   (UYPE-) UNIV PENNSYLVANIA.
XX
PI   Siegel DL;
XX
DR   WPI; 2001-388931/41.
DR   N-PSDB; AAH68641.
XX
PT   New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT   diagnostics requiring a human instead of an animal antibody and in
PT   therapeutic medicine -
XX
```

```
PS   Claim 1; Column 43; 162pp; English.
XX
CC   The present invention describes an isolated Rh(D) binding protein,
CC   preferably a human antibody, (I) having an amino acid sequence comprising
CC   one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC   immunostimulant activity, and can be used as an immune system stimulant.
CC   (I) can be used in diagnostics and therapeutic medicine. The antibodies
CC   are used in diagnostics that require human antibodies instead of animal
CC   antibodies, such as determine the Rh phenotype of human red blood cells.
CC   AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC   AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC   chain CDR3 amino acid sequences which are given in the exemplification
CC   of the present invention.
XX
SQ   Sequence   127 AA;

Query Match             93.3%;  Score 643;  DB 22;  Length 127;
Best Local Similarity   95.4%;  Pred. No. 1.3e-50;
Matches 125;  Conservative   0;  Mismatches   2;  Indels   4;  Gaps   1;

Qy    1  EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT  60
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Db    1  EVQLL----ESGGGLVKPGGSLRLSCAASGFTFSSYSMHVRQGPGKGLEWVSSISNSNT  56

Qy   61  YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
         |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   57  YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDSRYSNFLRWVRSDGMDV 116

Qy  121  WGQGTTVIVSS 131
         |||||||||||
Db  117  WGQGTTVIVSS 127


RESULT 3
ABP45307
ID   ABP45307 standard; Protein; 256 AA.
XX
AC   ABP45307;
XX
DT   19-AUG-2002 (first entry)
XX
DE   Human BLyS binding scFv SEQ ID 1318.
XX
KW   BLyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW   tumour necrosis factor; B cell proliferation; B cell differentiation;
KW   immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO20202641-A1.
XX
PD   10-JAN-2002.
XX
PF   15-JUN-2001;  2001WO-US19110.
XX
PR   16-JUN-2000;  2000US-2122210P.
PR   17-OCT-2000;  2000US-2408160P.
PR   16-MAR-2001;  2001US-2762480P.
PR   21-MAR-2001;  2001US-2773790P.
PR   25-MAY-2001;  2001US-293499P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR   WPI; 2002-114799/15.
XX
PT   Antibodies against B lymphocyte stimulating polypeptides, useful for
PT   the diagnosis and treatment of cancers and immune disorders -
XX
```

RESULT 4
ABP44902
ID   ABP44902 standard; Protein; 248 AA.
XX
AC   ABP44902;
XX
DT   19-AUG-2002 (first entry)
XX
DE   Human BLyS binding scFv SEQ ID 913.
XX
KW   BLyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW   tumour necrosis factor; B cell proliferation; B cell differentiation;
KW   immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO2002026641-A1.
XX
PD   10-JAN-2002.
XX
PF   15-JUN-2001; 2001WO-US19110.
XX
PR   16-JUN-2000; 2000US-212210P.
PR   17-OCT-2000; 2000US-240816P.
PR   16-MAR-2001; 2001US-276248P.
PR   21-MAR-2001; 2001US-277379P.
PR   25-MAY-2001; 2001US-293499P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX
PS   Claim 1; Page 1975-1976; 3148pp; English.
XX
CC   This invention describes novel antibodies that immunospecifically bind to
CC   B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC   tumour necrosis factor (TNF) super family and induces B cell
CC   proliferation and differentiation. The antibodies of the invention have
CC   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC   antirheumatic and antiAIDS activity and can be used in vaccines to
CC   inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC   and so may be used to detect and quantitate the presence of BLyS in
CC   biological samples and may be used in this way to diagnose disease
CC   associated with aberrant expression of BLyS. They may also be
CC   administered to treat diseases associated with aberrant BLyS expression
CC   and activity such as cancer, immune, and autoimmune disorders and
CC   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC   acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC   the antibodies and fragments of the antibodies described in the method
CC   of the invention.
XX
SQ   Sequence 256 AA;

Query Match   74.2%; Score 511.5; DB 23; Length 256;
Best Local Similarity 78.2%; Pred. No. 2.1e-38;
Matches 104; Conservative 11; Mismatches 11; Indels 7; Gaps 3;

Qy   1   EVQLLESGVESGGGLVKRPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
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Db   1   EVQL---VQSGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISNSSS 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARD-SRYSNFLRWVRSD--G 117
             ||||::||||||||||||||||||||||||||||:|||| :||:|||||||||::
Db   57 YIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLGSFYDILTALRLENYG 116

Qy   118 MDVWGQGTTVIVS 130
             |||||:|||| ||
Db   117 MDVWGKGTLVTVS 129

XX
PI   Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR   WPI; 2002-114799/15.
XX
PT   Antibodies against B Lymphocyte stimulating polypeptides, useful for
PT   the diagnosis and treatment of cancers and immune disorders -
XX
PS   Claim 1; Page 1491-1492; 3148pp; English.
XX
CC   This invention describes novel antibodies that immunospecifically bind to
CC   B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC   tumour necrosis factor (TNF) super family and induces B cell
CC   proliferation and differentiation. The antibodies of the invention have
CC   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC   antirheumatic and antiAIDS activity and can be used in vaccines to
CC   inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC   and so may be used to detect and quantitate the presence of BLyS in
CC   biological samples and may be used in this way to diagnose disease
CC   associated with aberrant expression of BLyS. They may also be
CC   administered to treat diseases associated with aberrant BLyS expression
CC   and activity such as cancer, immune, and autoimmune disorders and
CC   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC   acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC   the antibodies and fragments of the antibodies described in the method
CC   of the invention.
XX
SQ   Sequence 248 AA;

RESULT 5
AAY06717
ID   AAY06717 standard; Protein; 245 AA.
XX
AC   AAY06717;
XX
DT   17-JUN-1999 (first entry)
XX
DE   Antibody 12B5 single chain Fv (scFv) fragment.
XX
KW   Agonist antibody; thrombopoietin receptor; TPO-R; thrombopoietin; DIC;
KW   megakaryocyte; platelet; immunological; hematopoietic; thrombocytopenia;
KW   bone marrow hypoplasia; disseminated intravascular coagulation; anemia;
KW   myelodysplasia; myelotoxic chemotherapy; leukaemia; tumour; MuSK; CDR;
KW   neuromuscular; muscular dystrophy; complementarity determining region.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   Misc-difference 208
FT   /note= "unspecified"
XX
PN   WO9910494-A2.
XX
PD   04-MAR-1999.
XX

Query Match   73.9%; Score 509; DB 23; Length 248;
Best Local Similarity 78.6%; Pred. No. 3.4e-38;
Matches 103; Conservative 8; Mismatches 14; Indels 6; Gaps 2;

Qy   1   EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
             |||| |:||||||||||||||||||||||||||||||||:||||||||||||||:
Db   1   EVQL----VESGGGLVQPGGSLRLSCAAFGFTFSSYSMNWVRQAPGKGLEWVSSISNRGS 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGDMDV 120
             ||||::||||||||||||||||:||||||||||||:|||||||| :||:||||| :
Db   57 YIYYADSVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYCAREGR--DILTGVYYGLDV 114

Qy   121 WGQGTTVIVSS 131
             ||||| | ||
Db   115 WGQGTLVTVSS 125

PF   21-AUG-1998; 98WO-US17364.
XX
PR   25-AUG-1997; 97US-0918148.
XX
PA   (GETH) GENENTECH INC.
XX
PI   Adams CW, Carter PJ, Fendly BM, Gurney AL;
XX
DR   WPI; 1999-204666/17.
XX
PS   Disclosure; Fig 1; 86pp; English.
XX
CC   The invention relates to an agonist antibody (AB) which binds to a
CC   thrombopoietin receptor agonist antibodies - useful for
CC   treating immunological or hematological disorders
CC   New thrombopoietin receptor (TPO-R). The antibodies which bind the TPO-R can
CC   be used in the same way and for the same indications as thrombopoietin
CC   (TPO). They can stimulate proliferation, differentiation or growth of
CC   megakaryocytes. They may also be able to stimulate megakaryocytes to
CC   increase platelet production. They can be used for treating
CC   immunological or hematopoietic disorders, especially thrombocytopenia.
CC   Thrombocytopenia -associated bone marrow hypoplasia (e.g. aplastic anemia
CC   following chemotherapy or bone marrow transplant) may be effectively
CC   treated with the antibody compounds as well as disorders such as
CC   disseminated intravascular coagulation (DIC), immune thrombocytopenia
CC   (HIV-induced and non HIV-induced), chronic idiopathic thrombocytopenia,
CC   congenital thrombocytopenia, thrombotic thrombocytopenia and
CC   myelodysplasia. They can also be used in e.g. myelotoxic chemotherapy for
CC   treatment of solid tumours or leukaemia, myeloablative chemotherapy for
CC   autologous or allogeneic bone marrow transplant, myelodysplasia,
CC   idiopathic aplastic anemia, congenital thrombocytopenia, and immune
CC   thrombocytopenia. The antibodies which bind to the MuSK receptor can be
CC   used for improving neuromuscular function in a patient, e.g. in muscular
CC   dystrophy. The products can also be used for detection and diagnosis. The
CC   antibodies have a longer half-life than the natural ligand for the TPO-R.
CC   Sequences AAY06713-Y06718 represent single chain Fv (scFV) fragments of
CC   various antibodies.
XX
SQ   Sequence   245 AA;
XX

Query Match   73.7%; Score 507.5; DB 20; Length 245;
Best Local Similarity 77.9%; Pred. No. 4.6e-38;
Matches 102; Conservative   9; Mismatches   7; Indels   13; Gaps   2;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAAASGFTFSSYSMHWVRQSPGKGLEWVSSISNSNT 60
          :||| |||||||||||||||||||||||||||||||:|:||||||||||||:|:||:::
Db   3 QVQL----VESGGGLVKPGGSLRLSCAASGTFFSSHNMNWVRQAPGKGLEWVSSISSSSS 58

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
          |||||:||:||||||||||||||||||||||||| |||||||||||| ||
Db   59 YIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDR-------GSTGMDV 109

Qy   121 WGQGTTVIVSS 131
          ||:||| ||||
Db   110 WGRGTLVTVSS 120

KW   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO200202641-A1.
XX
PD   10-JAN-2002.
XX
PF   15-JUN-2001; 2001WO-US19110.
XX
PR   16-JUN-2000; 2000US-2122210P.
PR   17-OCT-2000; 2000US-2408160P.
PR   16-MAR-2001; 2001US-276248P.
PR   21-MAR-2001; 2001US-277379P.
PR   25-MAY-2001; 2001US-2934990P.
XX
PI   Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR   WPI; 2002-114799/15.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PT   Antibodies against B Lymphocyte Stimulating polypeptides, useful for
PT   the diagnosis and treatment of cancers and immune disorders -
XX
PS   Claim 1; Page 2507-2508; 3148pp; English.
XX
CC   This invention describes novel antibodies that immunospecifically bind to
CC   B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC   tumour necrosis factor (TNF) super family and induces B cell
CC   proliferation and differentiation. The antibodies of the invention have
CC   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC   antirheumatic and antiAIDS activity and can be used in vaccines to
CC   inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC   and so may be used to detect and quantitate the presence of BLyS in
CC   biological samples and may be used in this way to diagnose disease
CC   associated with aberrant expression of BLyS. They may also be
CC   administered to treat diseases associated with aberrant BLyS expression
CC   and activity such as cancer, immune, and autoimmune disorders and
CC   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC   acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC   the antibodies and fragments of the antibodies described in the method
CC   of the invention.
XX
SQ   Sequence   247 AA;
XX

Query Match   73.5%; Score 506.5; DB 23; Length 247;
Best Local Similarity 78.6%; Pred. No. 5.7e-38;
Matches 103; Conservative 10; Mismatches 11; Indels   7; Gaps   3;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
          :|| |||||||||||||||||||||||||||||||||||||||||||||||||||:|:::
Db   1 QVQL----VQSGGGLVKPGGSLRLSCAASGTFFSSYSMMNWVRQAPGKGLEWVSSISSSSS 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
          |||||:||:||||||||||||||||||||||||| |||||||||| :: |||||||
Db   57 YIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARD-EYDILTGLLQ--GMDV 113

Qy   121 WGQGTTVIVSS 131
          ||:||| ||||
Db   114 WGKGTLVTVSS 124

RESULT 6
ID   ABP45753 standard; Protein; 247 AA.
XX
AC   ABP45753;
XX
DT   19-AUG-2002 (first entry)
XX
DE   Human BLyS binding scFv SEQ ID 1764.
XX
KW   BLyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW   tumour necrosis factor; B cell proliferation; B cell differentiation;
KW   immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

RESULT 7
ID   AAE28870 standard; Protein; 116 AA.
XX
AC   AAE28870;
XX
DT   27-DEC-2002 (first entry)
XX

DE   Human KDR (VEGFR-2) Fab heavy chain protein from D2C6 and D1H4 clone.
XX
KW   Human; tumour; vascular endothelial growth factor receptor; metastasis;
KW   epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC;
KW   breast; VEGF; heart; EGFR; therapy; invasiveness; heavy chain; VH.
XX
OS   Homo sapiens.
XX
PN   WO200270008-A1.
XX
PD   12-SEP-2002.
XX
PF   04-MAR-2002; 2002WO-US06762.
XX
PR   02-MAR-2001; 2001US-0798689.
XX
PA   (IMCL-) IMCLONE SYSTEMS INC.
PA   (ROCK/) ROCKWELL P.
PA   (GOLD/) GOLDSTEIN N I.
XX
DR   WPI; 2002-691738/74.
DR   N-PSDB; AAD46290, AAD46292.
XX
PS   Example 9; Page 123; 151pp; English.
XX
PT   Inhibiting tumor growth in humans involves administering vascular
PT   endothelial growth factor receptor antagonists in combination with
PT   radiation, chemotherapeutic agents, or epidermal growth factor receptor
PT   antagonists -
XX
CC   The invention relates to a method of inhibiting tumour growth which
CC   involves administering, vascular endothelial growth factor receptor
CC   (VEGFR) antagonists in combination with radiation, chemotherapeutic
CC   agent, or epidermal growth factor receptor (EGFR) antagonist. The method
CC   is useful for inhibiting tumour growth in a human, where the tumour (e.g.
CC   tumour of the breast, heart, lung, small intestine, colon, spleen, bone,
CC   kidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin,
CC   bone marrow, blood, thymus, uterus, testicles, cervix or liver) over
CC   expresses VEGFR. It is also useful for inhibiting growth of colon tumour
CC   or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR.
CC   It is preferably useful for treating subjects with both solid tumours,
CC   preferably high vascular tumours and non-solid tumours. The inhibition
CC   or reduction of tumour growth includes prevention or inhibition of the
CC   progression of tumour, including cancerous and non-cancerous tumours,
CC   where the progression of tumours includes the invasiveness, metastasis,
CC   recurrence and increase in size of the tumour. The present sequence is
CC   human KDR (VEGFR-2) Fab antibody heavy chain protein.
XX
SQ   Sequence   116 AA;

Query Match   73.2%; Score 504.5; DB 23; Length 116;
Best Local Similarity   77.1%; Pred. No. 3.8e-38;
Matches 101; Conservative   8; Mismatches   7; Indels 15; Gaps   2;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSSYSMHWVRQGPGKGLEWVSSISNSNT 60
              |||:||||||||||||||||||||||||||||||||||||||:|:||| ||||||||::::
Db   1 EVQL---VQSGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSS 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWYRSDGMDV 120
              |||||| :|||||||||||||||||||||||||||:| |:
Db   57 YIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR-----------VTDAFDI 105

Qy   121 WGQGTTVIVSS 131
              ||||| | |||
Db   106 WGQGTMVTVSS 116

ID   ABJ26763 standard; Protein; 116 AA.
XX
AC   ABJ26763;
XX

DT   01-MAY-2003 (first entry)
XX
DE   VEGF binding related protein SEQ ID NO 76.
XX
KW   Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;
KW   leukaemia cell; vascular endothelial growth factor; tumour;
KW   bispecific antigen-binding protein; human.
XX
OS   Homo sapiens.
XX
PN   WO2003002144-A1.
XX
PD   09-JAN-2003.
XX
PF   26-JUN-2002; 2002WO-US20332.
XX
PR   26-JUN-2001; 2001US-301299P.
XX
PA   (IMCL-) IMCLONE SYSTEMS INC.
XX
PI   Zhu 2;
XX
DR   WPI; 2003-201468/19.
DR   N-PSDB; ABT23325.
XX
PS   Claim 15; Page 70-71; 98pp; English.
XX
PT   New bispecific antibodies having antigen-binding sites specific for a
PT   first vascular endothelial growth factor (VEGF) receptor and for a
PT   second VEGF receptor, useful for inhibiting migration of leukemia
PT   cells, or for treating tumors -
XX
CC   The invention relates to a novel antibody having a first antigen binding
CC   site specific for a first vascular endothelial growth factor (VEGF)
CC   receptor and a second antigen-binding site specific for a second VEGF
CC   receptor. The bispecific antigen-binding proteins block activation of the
CC   VEGF receptor and are useful for reducing or inhibiting VEGF-induced
CC   cellular functions such as mitogenesis of vascular endothelial cells
CC   and migration of leukaemia cells. The antibodies are useful for treating
CC   tumours and for in vivo or in vitro for investigative and diagnostic
CC   methods. This sequence represents a human protein relating to the
CC   bispecific antibodies that bind to the VEGF receptors of the invention.
XX
SQ   Sequence   116 AA;

Query Match   73.2%; Score 504.5; DB 24; Length 116;
Best Local Similarity   77.1%; Pred. No. 3.8e-38;
Matches 101; Conservative   8; Mismatches   7; Indels 15; Gaps   2;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSSYSMHWVRQGPGKGLEWVSSISNSNT 60
              |||:||||||||||||||||||||||||||||||||||||||:|:||| ||||||||::::
Db   1 EVQL---VQSGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSS 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWYRSDGMDV 120
              |||||| :|||||||||||||||||||||||||||:| |:
Db   57 YIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR-----------VTDAFDI 105

Qy   121 WGQGTTVIVSS 131
              ||||| | |||
Db   106 WGQGTMVTVSS 116

ID   AAE28873 standard; Protein; 116 AA.
XX
AC   AAE28873;
XX
DT   27-DEC-2002 (first entry)
XX
DE   Human KDR (VEGFR-2) Fab heavy chain (VH) protein from D2H2 clone.
XX
KW   Human; tumour; vascular endothelial growth factor receptor; metastasis;

KW epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC;
KW breast; VEGFR; heart; EGFR; therapy; invasiveness; heavy chain; VH.
XX
OS Homo sapiens.
XX
XX
PN WO200270008-A1.
XX
XX
PD 12-SEP-2002.
XX
XX
PF 04-MAR-2002; 2002WO-US06762.
XX
PR 02-MAR-2001; 2001US-0798689.
XX
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
PA (ROCK/) ROCKWELL P.
PA (GOLD/) GOLDSTEIN N I.
XX
DR WPI; 2002-691738/74.
DR N-PSDB; AAD46294.
XX
XX
PS Example 12; Page 127; 151pp; English.
XX
PT The invention relates to a method of inhibiting tumour growth which
PT involves administering vascular endothelial growth factor receptor
PT (VEGFR) antagonists in combination with radiation, chemotherapeutic
PT agent, or epidermal growth factor receptor (EGFR) antagonist. The method
PT is useful for inhibiting tumour growth in a human, where the tumour (e.g.
PT tumour of the breast, heart, lung, small intestine, colon, spleen, bone,
PT kidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin,
PT bone marrow, blood, thymus, uterus, testicles, cervix or liver) over
PT expresses VEGFR. It is also useful for inhibiting growth of colon tumour
PT or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR.
PT It is preferably useful for treating subjects with both solid tumours,
PT preferably high vascular tumours and non-solid tumours. The inhibition
PT or reduction of tumour growth includes prevention or inhibition of the
PT progression of tumour, including cancerous and non-cancerous tumours,
PT where the progression of tumours includes the invasiveness, metastasis,
PT recurrence and increase in size of the tumour. The present sequence is
PT human KDR (VEGFR-2) Fab antibody heavy chain protein.
XX
SQ Sequence 116 AA;

Query Match   72.5%; Score 499.5; DB 23; Length 116;
Best Local Similarity   76.3%; Pred. No. 1.1e-37;
Matches 100; Conservative 9; Mismatches 7; Indels 15; Gaps 2;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
               |.|| | :||||||||||||||||||||.||||.||||||| :||:||||||||| :::
Db   1 EVQL----VQSGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSS 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
               ||||||:||||||||||||||||:||||||||| ||||||||| : |:
Db   57 YIYYADSVKGRFTISRDNAKDSLILQMNSLRAEDTAVYYCAR-------------VTDAFDI 105

Qy   121 WGQGTTVIVSS 131
               |||| | |||
Db   106 WGQGTMVTVSS 116

XX
KW Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;
KW leukaemia cell; vascular endothelial growth factor; tumour;
KW bispecific antigen-binding protein; human.
XX
OS Homo sapiens.
XX
XX
PN WO200302144-A1.
XX
XX
PD 09-JAN-2003.
XX
XX
PF 26-JUN-2002; 2002WO-US20332.
XX
PR 26-JUN-2001; 2001US-30129P9P.
XX
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
XX
DR WPI; 2003-201468/19.
DR N-PSDB; ABT23330.
XX
XX
PI Zhu J;
XX
PS Claim 15; Page 74; 98pp; English.
XX
PT The invention relates to a novel antibody having a first antigen binding
PT site specific for a first vascular endothelial growth factor (VEGF)
PT receptor and a second antigen-binding site specific for a second VEGF
PT receptor. The bispecific antigen-binding proteins block activation of the
PT VEGF receptor and are useful for reducing or inhibiting VEGF-induced
PT cellular functions such as mitogenesis of vascular endothelial cells
PT and migration of leukaemia cells. The antibodies are useful for treating
PT tumours and for in vivo or in vitro for investigative and diagnostic
PT methods. This sequence represents a human protein relating to the
PT bispecific antibodies that bind to the VEGF receptors of the invention.
XX
XX
SQ Sequence 116 AA;

Query Match   72.5%; Score 499.5; DB 24; Length 116;
Best Local Similarity   76.3%; Pred. No. 1.1e-37;
Matches 100; Conservative 9; Mismatches 7; Indels 15; Gaps 2;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
               |.|| | :||||||||||||||||||||.||||.||||||| :||:||||||||| :::
Db   1 EVQL----VQSGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSS 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
               ||||||:||||||||||||||||:||||||||| ||||||||| : |:
Db   57 YIYYADSVKGRFTISRDNAKDSLILQMNSLRAEDTAVYYCAR-------------VTDAFDI 105

Qy   121 WGQGTTVIVSS 131
               |||| | |||
Db   106 WGQGTMVTVSS 116

RESULT 11
ABP45845
ID   ABP45845 standard; Protein; 249 AA.
XX
AC   ABP45845;
XX
DT   19-AUG-2002 (first entry)
XX
DE   Human BLyS binding scFv SEQ ID 1856.
XX
KW   BLyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW   tumour necrosis factor; B cell proliferation; B cell differentiation;
KW   immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;

RESULT 10
ABJ26766
ID   ABJ26766 standard; Protein; 116 AA.
XX
AC   ABJ26766;
XX
DT   01-MAY-2003 (first entry)
XX
DE   VEGF binding related protein SEQ ID NO 83.

RESULT 12
ABG77142
ID   ABG77142 standard; protein; 125 AA.
XX
AC   ABG77142;
XX
DT   24-OCT-2002 (first entry)

KW   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO2002026641-A1.
XX
PD   10-JAN-2002.
XX
PF   15-JUN-2001; 2001WO-US19110.
XX
PR   16-JUN-2000; 2000US-212210P.
PR   17-OCT-2000; 2000US-240816P.
PR   16-MAR-2001; 2001US-276248P.
PR   21-MAR-2001; 2001US-277379P.
PR   25-MAY-2001; 2001US-293499P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR   WPI; 2002-114799/15.
XX
PT   Antibodies against B Lymphocyte stimulating polypeptides, useful for
PT   the diagnosis and treatment of cancers and immune disorders -
XX
PS   Claim 1; Page 2616-2617; 3148pp; English.
XX
CC   This invention describes novel antibodies that immunospecifically bind to
CC   B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC   tumour necrosis factor (TNF) super family and induces B cell
CC   proliferation and differentiation. The antibodies of the invention have
CC   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC   antirheumatic and antiAIDS activity and can be used in vaccines to
CC   inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC   and so may be used to detect and quantitate the presence of BLyS in
CC   biological samples and may be used in this way to diagnose disease
CC   associated with aberrant expression of BLyS. They may also be
CC   administered to treat diseases associated with aberrant BLyS expression
CC   and activity such as cancer, immune, and autoimmune disorders and
CC   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC   acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC   the antibodies and fragments of the antibodies described in the method
CC   of the invention.
XX
SQ   Sequence 249 AA;

Query Match   72.5%; Score 499.5; DB 23; Length 249;
Best Local Similarity   78.6%; Pred. No. 2.5e-37;
Matches 103; Conservative   7; Mismatches 14; Indels   7; Gaps 3;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
              ||||| |||| | |||||||||||||||||||||||||||| |||||||||| ||:|:::
Db   1 EVQL----VESGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSS 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
              |||||| ||||||||||||||||||||||||||||: :|| ||||
Db   57 YIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR-GRYDILTGYFTS--FDY 113

Qy   121 WGQGTTVIVSS 131
              |||||| |||
Db   114 WGQGTLVTVSS 124

DE   Anti-IGF-IR antibody (4.9.2) variable region heavy chain protein.
XX
KW   Insulin-like growth factor I receptor; antibody; human;
KW   cytostatic; osteopathic; antiatherosclerotic; antipsoriatic;
KW   IGF-IR; tumour; anti-neoplastic; anti-tumour; anti-angiogenic;
KW   neuropathy; osteoporosis; acromegaly; gigantism; psoriasis;
KW   atherosclerosis.
XX
OS   Homo sapiens.
XX
PN   WO200253596-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-US51113.
XX
PR   05-JAN-2001; 2001US-259927P.
XX
PA   (PFIZ) PFIZER INC.
PA   (ABGE-) ABGENIX INC.
XX
PI   Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;
XX
DR   WPI; 2002-575410/61.
DR   N-PSDB; ABS62704.
XX
PT   Novel humanised, chimeric monoclonal antibody that specifically binds
PT   to insulin-like growth factor I (IGF-1) receptor useful for inhibiting
PT   binding of IGF-I or IGF-II to receptor and for treating cancer in
PT   humans -
XX
PS   Claim 13; Page 130; 172pp; English.
XX
CC   This invention relates to a novel humanised, chimeric or human
CC   monoclonal antibody or its antigen binding portion that specifically
CC   binds to insulin-like growth factor I receptor (IGF-IR). The antibodies
CC   of the invention can act as an inhibitor of binding of IGF-I or IGF-II
CC   with IGF-IR and can inhibit in vivo tumour growth and IGF-IR tyrosine
CC   phosphorylation. The antibodies of the invention are useful for
CC   diagnosing the presence or location of an IGF-IR-expressing tumour in a
CC   subject. The antibody or its antigen-binding portion is also useful for
CC   treating cancer in a human. The method for this further involves an anti
CC   neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent.
CC   The antibodies may also be useful for increasing IGF-IR activity and
CC   thus restoring IGF-IR activity in a condition characterised by low
CC   IGF-IR levels e.g. neuropathy or osteoporosis. An antibody of the
CC   invention is also useful for inducing apoptosis of specific cells in a
CC   patient, and to treat non-cancerous states or disease, e.g. acromegaly,
CC   gigantism, psoriasis and atherosclerosis. Fully human anti-IGF-IR
CC   antibodies minimise the immunogenic and allergic responses intrinsic to
CC   mouse or mouse-derivatised monoclonal antibodies and thus increase the
CC   efficacy and safety of the administered antibodies. The present sequence
CC   represents an anti-insulin-like growth factor I receptor antibody of the
CC   invention.
XX
SQ   Sequence 125 AA;

Query Match   72.4%; Score 499; DB 23; Length 125;
Best Local Similarity   76.3%; Pred. No. 1.3e-37;
Matches 100; Conservative   9; Mismatches 16; Indels   6; Gaps 2;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
              ||||| |||| | ||||||||||||||||||||||||:||:||||||||||:|:
Db   1 EVQL----ESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGG 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
              |||||| |||||||||||:|||:|||||||||||| :|| : |
Db   57 YIYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDLGYGDFYYYY--GMDV 114

Qy   121 WGQGTTVIVSS 131
              |||||| |||
Db   115 WGQGTTVTVSS 125

RESULT 13
ABP45926
ID   ABP45926 standard; Protein; 241 AA.
XX
AC   ABP45926;
XX
DT   19-AUG-2002 (first entry)
XX
DE   Human BlyS binding scFv SEQ ID 1937.
XX
KW   BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW   tumour necrosis factor; B cell proliferation; B cell differentiation;
KW   immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO20020202641-A1.
XX
PD   10-JAN-2002.
XX
PF   15-JUN-2001; 2001WO-US19110.
XX
PR   16-JUN-2000; 2000US-212210P.
PR   17-OCT-2000; 2000US-240816P.
PR   16-MAR-2001; 2001US-276248P.
PR   21-MAR-2001; 2001US-277379P.
PR   25-MAY-2001; 2001US-293499P.
XX
PF   15-JUN-2001; 2001WO-US19110.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR   WPI; 2002-114799/15.
XX
PT   Antibodies against B Lymphocyte Stimulating polypeptides, useful for
PT   the diagnosis and treatment of cancers and immune disorders -
XX
PS   Claim 1; Page 2712-2713; 3148pp; English.
XX
CC   This invention describes novel antibodies that immunospecifically bind to
CC   B Lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
CC   tumour necrosis factor (TNF) super family and induces B cell
CC   proliferation and differentiation. The antibodies of the invention have
CC   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC   antirheumatic and antiAIDS activity and can be used in vaccines to
CC   inhibit the expression and activity of BlyS. The antibodies bind to BlyS
CC   and so may be used to detect and quantitate the presence of BlyS in
CC   biological samples and may be used in this way to diagnose disease
CC   associated with aberrant expression of BlyS. They may also be
CC   administered to treat diseases associated with aberrant BlyS expression
CC   and activity such as cancer, immune, and autoimmune disorders and
CC   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC   acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC   the antibodies and fragments of the antibodies described in the method
CC   of the invention.
XX
SQ   Sequence   241 AA;

Query Match   72.3%; Score 498; DB 23; Length 241;
Best Local Similarity   77.7%; Pred. No. 3.3e-37;
Matches 101; Conservative 7; Mismatches 8; Indels 14; Gaps 2;

Qy   2 VOLLEGSGVEESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNTY   61
                 |:|||| ||||| :||:||||||||||||||||||||||||||||||||||||||||||:||
Db   2 VQSGGGLVKSGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSY   57

RESULT 14
ABP45692
ID   ABP45692 standard; Protein; 247 AA.
XX
AC   ABP45692;
XX
DT   19-AUG-2002 (first entry)
XX
DE   Human BlyS binding scFv SEQ ID 1703.
XX
KW   BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW   tumour necrosis factor; B cell proliferation; B cell differentiation;
KW   immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO20020202641-A1.
XX
PD   10-JAN-2002.
XX
PF   15-JUN-2001; 2001WO-US19110.
XX
PR   16-JUN-2000; 2000US-212210P.
PR   17-OCT-2000; 2000US-240816P.
PR   16-MAR-2001; 2001US-276248P.
PR   21-MAR-2001; 2001US-277379P.
PR   25-MAY-2001; 2001US-293499P.
XX
PF   15-JUN-2001; 2001WO-US19110.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR   WPI; 2002-114799/15.
XX
PT   Antibodies against B Lymphocyte Stimulating polypeptides, useful for
PT   the diagnosis and treatment of cancers and immune disorders -
XX
PS   Claim 1; Page 2434-2435; 3148pp; English.
XX
CC   This invention describes novel antibodies that immunospecifically bind to
CC   B Lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
CC   tumour necrosis factor (TNF) super family and induces B cell
CC   proliferation and differentiation. The antibodies of the invention have
CC   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC   antirheumatic and antiAIDS activity and can be used in vaccines to
CC   inhibit the expression and activity of BlyS. The antibodies bind to BlyS
CC   and so may be used to detect and quantitate the presence of BlyS in
CC   biological samples and may be used in this way to diagnose disease
CC   associated with aberrant expression of BlyS. They may also be
CC   administered to treat diseases associated with aberrant BlyS expression
CC   and activity such as cancer, immune, and autoimmune disorders and
CC   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC   acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC   the antibodies and fragments of the antibodies described in the method
CC   of the invention.
XX
SQ   Sequence   247 AA;

Query Match   72.2%; Score 497.5; DB 23; Length 247;

Qy   62 IYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDVW 121
                 ||||:|:||||||||||||||||||||||||||||| ||||||||| |||||||||
Db   58 IYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDDTAVYYCARGHFY-----------GMDVW 107

Qy   122 GQGTTVIVSS 131
                 |:|| ||||| |||
Db   108 GRGTMVTVSS 117

```
Best Local Similarity   78.6%;  Pred. No. 3.7e-37;
Matches 103; Conservative  8; Mismatches  13; Indels   7; Gaps   3;

Qy      1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
          |||| ::|||| |||||||||||||||||||||||||||||||||||| |||||:::
Db      1 QVQL----VESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSISSSSS 56

Qy     61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
          |||||:||||||||||||||||||||||:|||||||||||||| |:|| | |||:||
Db     57 YIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCA-TLGYDILTGYRSD--DY 113

Qy    121 WGQGTTVIVSS 131
          ||::| |||
Db    114 WGKGTLVTVSS 124
```

```
RESULT 15
ABG77162
ID   ABG77162 standard; Protein; 473 AA.
XX
AC   ABG77162;
XX
DT   24-OCT-2002  (first entry)
XX
DE   Germline protein sequence of anti-IGF-1R antibody DP-35(3-11)/D3-3/JH6.
XX
KW   Insulin-like growth factor I receptor; antibody; human;
KW   cytostatic; osteopathic; antiatherosclerotic; antipsoriatic;
KW   IGF-IR; tumour; anti-neoplastic; anti-tumour; anti-angiogenic;
KW   neuropathy; osteoporosis; acromegaly; gigantism; psoriasis;
KW   atherosclerosis.
XX
OS   Homo sapiens.
XX
PN   WO200253596-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-US59927P.
XX
PR   05-JAN-2001; 2001US-259927P.
XX
PA   (PFIZ ) PFIZER INC.
PA   (ABGE-) ABGENIX INC.
XX
PI   Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;
XX
DR   WPI; 2002-575410/61.
XX
PT   Novel humanized, chimeric monoclonal antibody that specifically binds
PT   to insulin-like growth factor I (IGF-1) receptor (IGF-IR). The antibodies
PT   binding of IGF-I or IGF-II to receptor and for treating cancer in
PT   humans -
XX
PS   Disclosure; Figure 19D; 172pp; English.
XX
CC   This invention relates to a novel humanised, chimeric or human
CC   monoclonal antibody or its antigen binding portion that specifically
CC   binds to insulin-like growth factor I receptor (IGF-IR). The antibodies
CC   of the invention can act as an inhibitor of binding of IGF-I or IGF-II
CC   with IGF-IR and can inhibit in vivo tumour growth and IGF-IR tyrosine
CC   phosphorylation. The antibodies of the invention are useful for
CC   diagnosing the presence or location of an IGF-IR-expressing tumour in a
CC   subject. The antibody or its antigen-binding portion is also useful for
CC   treating cancer in a human. The method for this further involves an anti
CC   neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent.
CC   The antibodies may also be useful for increasing IGF-IR activity and
CC   thus restoring IGF-IR activity in a condition characterised by low
CC   IGF-IR levels e.g. neuropathy, or osteoporosis. An antibody of the
CC   invention is also useful for inducing apoptosis of specific cells in a
CC   patient, and to treat non-cancerous states or disease, e.g. acromegaly,
CC   gigantism, psoriasis and atherosclerosis. Fully human anti-IGF-IR
CC   antibodies minimise the immunogenic and allergic responses intrinsic to
CC   mouse or mouse-derivatised monoclonal antibodies and thus increase the
CC   efficacy and safety of the administered antibodies. The present sequence
CC   represents an anti-insulin-like growth factor I receptor antibody of the
CC   invention.
XX
SQ   Sequence 473 AA;

Query Match             72.1%;  Score 496.5;  DB 23;  Length 473;
Best Local Similarity   76.3%;  Pred. No. 9.4e-37;
Matches 103; Conservative  6; Mismatches  15; Indels  11; Gaps   3;

Qy      1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
          |||| ::|||| |||||||||||||||||||||||||||| |||||||:: :
Db     20 QVQL----VESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSISSSGS 75

Qy     61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWV---RSD 116
          :||| ||||||||||||||||||||||||||||| |||||||| |||||:|  |:
Db     76 TIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARVLR---FLEWLLYYYYYY 132

Qy    117 GMDVWGQGTTVIVSS 131
          ||||||||| |||
Db    133 GMDVWGQGTTVTVSS 147

Search completed: September 24, 2003, 06:26:49
Job time : 72 secs
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OM protein - protein search, using sw model

Run on: September 24, 2003, 05:55:00 ; Search time 39 seconds
                 (without alignments)
                 323.028 Million cell updates/sec

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Title: US-09-848-798A-28
Perfect score: 689
Sequence: 1 EVQLLESGVESGGGLVKPGG..........WVRSDGMDVWQGTTVISS 131

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database :   PIR_76:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	503	73.0	123	2	S26794	Ig heavy chain v r
2	494.5	71.8	141	2	S31669	Ig heavy chain v r
3	490	71.1	123	2	S31114	Ig heavy chain - h
4	485	70.4	125	2	S30531	Ig heavy chain v r
5	481	69.8	140	2	S31588	Ig heavy chain v r
6	479	69.5	143	2	S23624	Ig heavy chain v r
7	477.5	69.3	122	2	E36005	Ig heavy chain v r
8	475	68.9	117	2	C36005	Ig heavy chain v r
9	473	68.7	117	2	S34012	Ig heavy chain v r
10	473	68.7	160	2	S05271	Ig heavy chain pre
11	470.5	68.3	118	2	S31105	Ig heavy chain (su
12	470.5	68.3	128	2	S26790	Ig heavy chain v r
13	469.5	68.1	147	2	I37780	Ig variable region
14	469	68.0	128	2	S31108	Ig heavy chain v r
15	468.5	68.0	119	2	S48797	Ig heavy chain - h
16	468	67.9	119	2	F36005	Ig heavy chain v r
17	467.5	67.9	120	2	S48798	Ig heavy chain v r
18	467	67.8	119	2	S31107	Ig heavy chain - h
19	466	67.6	117	2	S78486	Ig heavy chain v r
20	465.5	67.6	128	2	S26786	Ig heavy chain v r
21	465	67.5	123	2	S30532	Ig heavy chain v r
22	464.5	67.4	114	2	S31120	Ig heavy chain v r
23	463.5	67.3	120	2	E46590	Ig heavy chain - h
24	463	67.2	98	2	S26940	Ig heavy chain v r
25	461	66.9	119	2	D36005	Ig heavy chain v r
26	461	66.9	152	2	B26471	Ig heavy chain pre
27	459	66.6	127	2	S19878	Ig heavy chain v r
28	458.5	66.5	128	2	S31595	Ig heavy chain v r
29	458	66.5	116	2	S21979	Ig heavy chain v-g
30	457.5	66.4	136	2	S31587	Ig heavy chain v r
31	456.5	66.3	124	2	S20782	Ig heavy chain v r
32	456	66.2	121	2	155673	Ig heavy chain - h
33	454	65.9	134	2	S31679	Ig heavy chain - h
34	453	65.7	138	2	S31666	Ig heavy chain v r
35	453	65.7	140	2	S31686	Ig heavy chain v r
36	452.5	65.7	114	2	S63390	Ig heavy chain v-g
37	452	65.6	121	2	S31118	Ig heavy chain v r
38	452	65.6	123	2	S31509	Ig heavy chain - h
39	451.5	65.5	110	2	S31116	Ig heavy chain - h
40	451.5	65.5	116	2	PH1652	Ig heavy chain v r
41	451.5	65.5	118	2	S17080	Ig heavy chain v r
42	451	65.5	134	2	S31116	Ig heavy chain v r
43	450	65.3	121	2	G36005	Ig heavy chain pre
44	449.5	65.2	121	2	S70442	Ig heavy chain v r
45	449	65.2	130	2	I37783	Ig variable region

ALIGNMENTS

RESULT 1
S26794
Ig heavy chain v region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
C;Accession: S26794
R;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
A;Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene f
Eur. J. Immunol. 22, 241-245, 1992
A;Reference number: S26786; MUID:92111632; PMID:1730251
A;Accession: S26794
A;Molecule type: mRNA
A;Status: preliminary
A;Residues: 1-123 <MOR>
A;Cross-references: EMBL:X61011
A;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.0%; Score 503; DB 2; Length 123;
Best Local Similarity 77.4%;
Matches 103; Conservative 8; Mismatches 10; Indels 12; Gaps 3;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
         |||| ||||||||||:||||||||||||||||||:|||||:|||||||||:|| :::
Db   1 EVQL:---VESGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYISSSS 56

Qy 61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAYYCARDSRY--SNFLRWVRSDGM 118
         |||||:|||||||||||:||||||||||||:|| :||||||:   :|
Db 57 TIYYADSVKGRFTISRDNAKNSLYLQMNSLRDEDTAVYYCARSIKYYDENY----GM 110

Qy 119 DVWGQGTTVIVSS 131
         ||||||||| |||
Db 111 DVWGQGTTVTVSS 123

RESULT 2
S31669
Ig heavy chain v region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31669
R;Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from t
A;Reference number: S31585
A;Accession: S31669
A;Molecule type: mRNA
A;Status: preliminary
A;Residues: 1-141 <CUI>
A;Cross-references: EMBL:Z14212; NID:g30959; PIDN:CAA78581.1; PID:g30960
C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

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Query Match                  71.8%;  Score 494.5;  DB 2;  Length 141;
Best Local Similarity        76.3%;  Pred. No. 3.2e-37;
Matches  100;  Conservative    8;  Mismatches   14;  Indels    9;  Gaps    2;

Qy      1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
          |||||||| |||||||||||||||||||||||||||||| :|||::|||||||||:|:|::
Db     20 EVQL----VESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSISSSSS 75

Qy     61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
          |||||::|||||||||||||||||||||||||||||||||||| |:
Db     76 YIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGRHLTG-----EKGYFDL 130

Qy    121 WGQGTTVIVSS 131
          ||||| | |||
Db    131 WGRGTLVIVSS 141
```

RESULT 3
S31114
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31114
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem
A;Reference number: S31104; MUID:92116804; PMID:1740665
A;Accession: S31114
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-123 <RAA>
A;Cross-references: EMBL:X62963
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

```
Query Match                  71.1%;  Score 490;  DB 2;  Length 123;
Best Local Similarity        74.8%;  Pred. No. 6.9e-37;
Matches   98;  Conservative    8;  Mismatches   17;  Indels    8;  Gaps    2;

Qy      1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
          |||||| ||||||||||||||||||||||||||||||| :|||::|||||||||:|:|::
Db      1 EVQLL----ESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGG 56

Qy     61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
          |||||::||||||||||||||||||||||||||||:|||||:
Db     57 STYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKASLYLRFLEWL----FDY 112

Qy    121 WGQGTTVIVSS 131
          ||||| | |||
Db    113 WGGGTLVIVSS 123
```

RESULT 4
S30531
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
C;Accession: S30531
R;Mariette, X.
submitted to the EMBL Data Library, October 1992
A;Reference number: S30520
A;Accession: S30531
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-125 <MAR>
A;Cross-references: EMBL:Z18317
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

```
Query Match                  70.4%;  Score 485;  DB 2;  Length 125;
Best Local Similarity        75.6%;  Pred. No. 2e-36;
Matches   99;  Conservative    8;  Mismatches   18;  Indels    6;  Gaps    2;

Qy      1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
          |||| |||||||||||||||||||||||||||||||| :|||::|||||||||:|:|::
Db      1 EVQL----VESGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWISYISSSSS 56

Qy     61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
          ||||||:|||||||||||||||||||||||||| |:||||::
Db     57 TIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARSRNYDS--SGYSHYFDY 114

Qy    121 WGQGTTVIVSS 131
          ||||| | |||
Db    115 WGGGTLVIVSS 125
```

RESULT 5
S31588
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31588
R;Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from t
A;Reference number: S31585
A;Accession: S31588
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140 <CUI>
A;Cross-references: EMBL:Z14200; NID:g30957; PIDN:CAA78569.1; PID:g30958
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

```
Query Match                  69.8%;  Score 481;  DB 2;  Length 140;
Best Local Similarity        73.3%;  Pred. No. 5.1e-36;
Matches   96;  Conservative   11;  Mismatches   14;  Indels   10;  Gaps    2;

Qy      1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
          |||||| |||||||||||||||||||||||||||||| :|||::|||||||||:|:|::
Db      1 EVQLL----ESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGG 60

Qy     61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
          ||||||:||||||||||||||||||||||||| |:|||||:
Db     76 STYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDHDYSNYIYF-----DY 129

Qy    121 WGQGTTVIVSS 131
          ||||| | |||
Db    130 WGGGTLVIVSS 140
```

RESULT 6
S23624
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S23624
R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A
J. Exp. Med. 175, 831-842, 1992
A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors fro
A;Reference number: S23623; MUID:92156804; PMID:1740065
A;Accession: S23624
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-143 <OLE>
A;Cross-references: EMBL:X59703; NID:g32012; PIDN:CAA42224.1; PID:g32013
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

RESULT 7
E36005
Ig heavy chain V region (M72) - human
C;Species: Homo sapiens (man)
C;Accession: E36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: E36005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-122 <SCH>
A;Cross-references: GB:M34030
C;Genetics:
A;Gene: GDB; IGHQ; IGHDY1
A;Cross-references: GDB:1118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
A;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match   69.5%;   Score 479; DB 2; Length 143;
Best Local Similarity 76.3%; Pred. No. 7.8e-36;
Matches 100; Conservative 7; Mismatches 10; Indels 14; Gaps 3;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
Db   1 EVQL----VESGGGLVQPGGSLRLSCAASGFTFSNYSMNWVRQAPGKGLEWVSISSSS 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
Db   57 TIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR-SGYR------GGDY 106

Qy 121 WGQGTTVIVSS 131
Db 107 WGQGTLVTVSS 117

RESULT 8
C36005
Ig heavy chain V region (30p1) - human
C;Species: Homo sapiens (man)
C;Accession: C36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: C36005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-119 <SCH>
A;Cross-references: GB:M18513

Query Match   74.0%;   Score 477.5; DB 2; Length 122;
Best Local Similarity 74.0%; Pred. No. 9e-36;
Matches 97; Conservative 10; Mismatches 15; Indels 9; Gaps 3;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
Db   1 QVQL----VESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGS 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
Db   57 NKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRHSSS---WYY--GMDV 111

Qy 121 WGQGTTVIVSS 131
Db 112 WGRGTLVTVSS 122

RESULT 9
S34012
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Accession: S34012; S30538
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
R;Mariette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A;Title: Nucleotidic sequence analysis of the variable domains of four human monoclon
A;Reference number: S34001; MUID:93209281; PMID:7681398
A;Accession: S34012
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-117 <MAR>
A;Cross-references: EMBL:Z18324
A;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;15-95/Domain: immunoglobulin homology <IMM>

Query Match   72.5%;   Score 475; DB 2; Length 119;
Best Local Similarity 72.5%; Pred. No. 1.5e-35;
Matches 95; Conservative 10; Mismatches 14; Indels 12; Gaps 2;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
Db   1 EVQL----ESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGG 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
Db   54 YIFYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGEYSYGF------ADY 106

Qy 121 WGQGTTVIVSS 131
Db 107 WGRGTLVTVSS 117

RESULT 10
S05271
Ig heavy chain precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Accession: S05271
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Aug-1996
R;Kishimoto, T.
submitted to the EMBL Data Library, March 1989
A;Reference number: S05270
A;Accession: S05271
A;Molecule type: mRNA
A;Residues: 1-160 <KIS1>
A;Cross-references: EMBL:X14584
A;Molecule type: mRNA
R;Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
Nucleic Acids Res. 17, 4385, 1989
A;Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains

Query Match   74.8%;   Score 473; DB 2; Length 117;
Best Local Similarity 74.8%; Pred. No. 2.2e-35;
Matches 98; Conservative 7; Mismatches 12; Indels 14; Gaps 3;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
Db   1 EVQL----VESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
Db   54 YIFYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGEYSYGF------ADY 106

Qy 121 WGQGTTVIVSS 131
Db 107 WGRGTLVTVSS 117

A;Reference number: S04601; MUID:89296497; PMID:2500644
A;Reference number: S04602
A;Molecule type: mRNA
A;Residues: 1-144 <KIS2>
A;Cross-references: EMBL:X14584
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-160/Product: Ig heavy chain (fragment) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

```
Query Match          68.7%;  Score 473;  DB 2;  Length 160;
Best Local Similarity   73.9%;
Matches  99;    Conservative   9;   Mismatches  14;   Indels  12;   Gaps  3;
                                    Pred. No. 3e-35;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT  60
         ||||| ||  ||||||| ||||||||||||||||:: :  :||:||:| |||||:|:  :
Db  20 EVQLL---ESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSAISGSGG   75

Qy  61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRS----DG 117
         : |||| :||||||||||||:||||||||||||: ||||||::            |  DG
Db  76 STYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK-----AVVRGVISYYYG  130

Qy 118 MDVWGQGTTVIVSS 131
        |||||||||||||
Db 131 MDVWGQGTTVIVSS 144
```

RESULT 11
S31105
Ig heavy chain (subclass IgM) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C;Accession: S31105
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schurman
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem
A;Reference number: S31105
A;Accession: S31104; MUID:92111633; PMID:1730252
A;Molecule type: mRNA
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-118 <RAA>
A;Cross-references: EMBL:X63081; NID:g32648; PIDN:CAA44803.1; PID:g32649
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

```
Query Match          68.3%;  Score 470.5;  DB 2;  Length 118;
Best Local Similarity   72.5%;          Pred. No. 3.6e-35;
Matches  95;    Conservative   7;   Mismatches  16;   Indels  13;   Gaps  2;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT  60
         :||        |||||||||||||||||||||:|  :|:||:| |||||| : : :
Db   1 QVQL-----VESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSAISSSGS  56

Qy  61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
         :|||| :|||||||||||:||:||||||||||: ||||||:          |:
Db  57 TIYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAGQ--------LGDDAFDI  107

Qy 121 WGQGTTVIVSS 131
        ||||| | |||
Db 108 WGQGTWTVSS  118
```

RESULT 12
S26790
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26790
R;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Eur. J. Immunol. 22, 241-245, 1992

A;Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene f
A;Reference number: S26786; MUID:92111632; PMID:1730251
A;Accession: S26790
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-128 <MOR>
A;Cross-references: EMBL:X61013; NID:g32798; PIDN:CAA43347.1; PID:g1335128
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

```
Query Match          68.3%;  Score 470.5;  DB 2;  Length 128;
Best Local Similarity   73.5%;          Pred. No. 4e-35;
Matches  97;    Conservative   7;   Mismatches  23;   Indels   5;   Gaps  2;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT  60
         :||        ||||||||||||||||||||||:||  :|:||:| |||||:|:||||||
Db   1 QVQL-----VESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSGS   56

Qy  61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDG-MD 119
         :|||| :||||||||||||||||||||||||||: ||||||:||           |  MD
Db  57 TIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDGEGWGLIYYY--GMDV  116

Qy 120 VWGQGTTVIVSS 131
         |||| | |||
Db 117 LWGRTLVTVSS  127
```

RESULT 13
I37780
Ig variable region (VDJ) (clone T20-11) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999
C;Accession: I37780; S25474
R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A;Title: Somatic diversification in the heavy chain variable region genes expressed b
A;Reference number: A36876; MUID:94119917; PMID:8290556
A;Accession: I37780
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-147 <RES>
A;Cross-references: EMBL:X67943; NID:g33578; PIDN:CAA48130.1; PID:g33579
A;Superfamily: immunoglobulin V region; immunoglobulin homology
F;28-111/Domain: immunoglobulin homology <IMM>

```
Query Match          68.1%;  Score 469.5;  DB 2;  Length 147;
Best Local Similarity   72.5%;          Pred. No. 5.7e-35;
Matches  95;    Conservative   9;   Mismatches  20;   Indels   7;   Gaps  2;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT  60
         ||||        ||||||||:|||||||||||||||  ||:||:| ||||| ||  ||:
Db  14 EVQL-----VESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKDGS   69

Qy  61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
           :|||| :|||||||||||||||||||||||||: ||||||:|||           GMDV
Db  70 EKIYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDGEGWGLYYY--GMDV  126

Qy 121 WGQGTTVIVSS 131
        |||||| | |||
Db 127 WGQGTWTVSS  137
```

RESULT 14
S31108
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31108
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schur
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comp
A;Reference number: S31104; MUID:92111633; PMID:1730252

A;Accession: S31108
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-119 <RAA>
A;Cross-references: EMBL:X62956
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match   68.1%;   Score 469;   DB 2;   Length 119;
Best Local Similarity   72.5%;
Matches   95;   Conservative   8;   Mismatches   16;   Indels   12;   Gaps   2;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
            ||||| ||||||||||||||||||||||||:|||| ||||||||||:||:
Db   1 EVQLL----ESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGG 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
            |||||||||||||||||||||||||||||||||||||||||||| : | | : |
Db   57 STYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDRRLTG------TFDY 108

Qy   121 WGQGTTVIVSS 131
            ||||| | |||
Db   109 WGQGTLVTVSS 119

RESULT 15
S48797
Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH6) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Sep-1998 #text_change 23-Jul-1999
C;Accession: S48797; S26893
R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Reference number: S48797
A;Accession: S48797
A;Molecule type: mRNA
A;Residues: 1-128 <MAH>
A;Cross-references: EMBL:Z46379; NID:g587147; PIDN:CAA86512.1; PID:g1340168
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26893
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z12350; NID:g932922; PIDN:CAA78220.1; PID:g932923
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match   68.0%;   Score 468.5;   DB 2;   Length 128;
Best Local Similarity   71.6%;
Matches   96;   Conservative   11;   Mismatches   18;   Indels   9;   Gaps   3;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
            |||||:|:|| |||||||||||||||||||||||| |||||||||||||||||:
Db   1 QVQL---VESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGS 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRY---SNFLRWVRSDG 117
            |||||:||||||||||||:|||||||||||||:|||||||:|| | ||| ||| |
Db   57 NKYYADSVKGRFTISRDNSKNTLYLYLQMNSLRAEDTAVYYCARDNYYDSGSYYYYY--G 114

Qy   118 MDVWGQGTTVIVSS 131
            |||||||||| |||
Db   115 MDVWGQGTTVTVSS 128

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OM protein - protein search, using sw model

Run on: September 24, 2003, 04:44:09 ; Search time 33 Seconds
                  (without alignments)
                  186.682 Million cell updates/sec

Title: US-09-848-798A-28
Perfect score: 689
Sequence: 1 EVQLLESGVESGGGLVKPGG.........WVRSDGMDVWGQGTTVVSS 131

Scoring table: BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	432.5	62.8	136	1	HV16_MOUSE	P01783 mus musculu
2	429.5	62.3	122	1	HV3G_HUMAN	P01768 homo sapien
3	424.5	61.6	114	1	HV3B_HUMAN	P01763 homo sapien
4	419	60.8	117	1	HV3C_HUMAN	P01764 homo sapien
5	407.5	59.1	122	1	HV3H_HUMAN	P01769 homo sapien
6	407.5	59.1	126	1	HV3K_HUMAN	P01772 homo sapien
7	406.5	59.0	122	1	HV3A_HUMAN	P01762 homo sapien
8	404	58.6	121	1	HV3J_HUMAN	P01771 homo sapien
9	402	58.3	120	1	HV3E_HUMAN	P01766 homo sapien
10	400	58.1	115	1	HV3F_HUMAN	P01767 homo sapien
11	397.5	57.7	116	1	HV3T_HUMAN	P01781 homo sapien
12	395	57.3	98	1	HV57_HUMAN	P18528 mus musculu
13	391.5	56.8	119	1	HV38_MOUSE	P01808 mus musculu
14	391	56.7	119	1	HV3I_HUMAN	P01770 homo sapien
15	390	56.6	117	1	HV35_HUMAN	P01785 canis famil
16	389.5	56.5	114	1	HV02_CANFA	P01784 canis famil
17	389.5	56.5	120	1	HV01_CANFA	P01782 homo sapien
18	388	56.3	123	1	HV3U_HUMAN	P01791 mus musculu
19	388	56.3	123	1	HV22_MOUSE	P01793 mus musculu
20	386.5	56.1	123	1	HV24_MOUSE	P19181 carassius a
21	386	56.0	116	1	HV05_CARAU	P01765 homo sapien
22	384	55.7	115	1	HV3D_HUMAN	P01792 mus musculu
23	383	55.6	123	1	HV23_MOUSE	P01787 mus musculu
24	383	55.6	123	1	HV18_MOUSE	P01794 mus musculu
25	381	55.3	116	1	HV25_MOUSE	P01779 homo sapien
26	380.5	55.2	111	1	HV3R_HUMAN	P01804 mus musculu
27	380	55.2	117	1	HV54_MOUSE	P18525 mus musculu
28	380	55.2	117	1	HV59_MOUSE	P18530 mus musculu
29	380	55.2	123	1	HV19_MOUSE	P01788 mus musculu
30	378	54.9	144	1	HV26_MOUSE	P01795 mus musculu
31	377.5	54.8	97	1	HV55_MOUSE	P18527 mus musculu
32	377	54.7	117	1	HV56_MOUSE	P18526 mus musculu
33	376.5	54.6	122	1	HV21_MOUSE	P01790 mus musculu
34	375	54.4	115	1	HV32_MOUSE	P01801 mus musculu
35	373	54.1	113	1	HV30_MOUSE	P01799 mus musculu
36	373	54.1	117	1	HV58_MOUSE	P18529 mus musculu
37	372.5	54.1	122	1	HV20_MOUSE	P01789 mus musculu
38	371.5	53.9	117	1	HV3O_HUMAN	P01776 homo sapien
39	371.5	53.9	119	1	HV3M_HUMAN	P01774 homo sapien
40	370.5	53.8	119	1	HV3N_HUMAN	P01775 homo sapien
41	370	53.7	117	1	HV41_MOUSE	P01811 mus musculu
42	369.5	53.6	119	1	HV37_MOUSE	P01807 mus musculu
42	369.5	53.6	119	1	HV40_MOUSE	P01810 mus musculu
43	367.5	53.3	119	1	HV39_MOUSE	P01809 mus musculu
44	367	53.3	118	1	HV27_MOUSE	P01796 mus musculu
45	366	53.1	113	1		

ALIGNMENTS

RESULT 1
HV16_MOUSE

ID   HV16_MOUSE   STANDARD;   PRT;   136 AA.
AC   P01783;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region MOPC 21 precursor (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
RN   [2]
RP   SEQUENCE OF 17-136.
RX   MEDLINE=77100368; PubMed=401950;
RA   Adetugbo K., Milstein C., Secher D.S.;
RT   "Molecular analysis of spontaneous somatic mutants.";
RL   Nature 265:299-304(1977).
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CC   or send an email to license@isb-sib.ch).
DR   EMBL; J00522; AAD15290.1; -.
DR   PIR; E90809; GIMS21.
DR   PDB; 1IGC; 03-JUN-95.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal; 3D-structure.
FT   NON_TER   1   1
FT   SIGNAL   <1   16
FT   CHAIN   17   136   IG HEAVY CHAIN V REGION MOPC 21.
FT   DOMAIN   120   136   JH4 SEGMENT.
FT   DOMAIN   115   119   D SEGMENT.
FT   DISULFID   38   112
FT   CONFLICT   75   78   HYAD -> DYAH (IN REF. 2).
FT   CONFLICT   89   90   DN -> ND (IN REF. 2).
FT   CONFLICT   115   115   W -> H (IN REF. 2).
FT   CONFLICT   120   120   Y -> W (IN REF. 2).
FT   NON_TER   136   136

SQ   SEQUENCE   136 AA; 15071 MW; 2276A98DdBF7016 CRC64;

Query Match   62.8%; Score 432.5; DB 1; Length 136;
Best Local Similarity   64.9%; Pred. No. 4.2e-36;
Matches 85; Conservative 16; Mismatches 19; Indels 11; Gaps 2;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
           ::||| |||||||||| ::|||| ::||||||||||||:||||:||||||::::
Db   17 DVQL---VESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAVISSGSS 72

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
           :||||||||||||||:|||||||||||||||||:||||||| |:|||||
Db   73 TLHYADPVKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCARWGNYPY------AMDY 125

Qy   121 WGQGTTVIVSS 131
           ||||:|:||||
Db   126 WGQGTSVTVSS 136

RESULT 2
ID   HV3G_HUMAN   STANDARD;   PRT;   122 AA.
AC   P01768;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-III region CAM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=81013859; PubMed=6774332;
RA   Lehman D.W., Putnam F.W.;
RT   "Amino acid sequence of the variable region of a human mu chain:
RT   location of a possible JH segment.";
RL   Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC   -!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
CC   PATIENT WITH MACROGLOBULINEMIA.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A02051; M3HUAM.
DR   HSSP; P01772; 2PB4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT   DOMAIN   1   112   IG-LIKE.
FT   MOD_RES   1   1   PYRROLIDONE CARBOXYLIC ACID.
SQ   SEQUENCE   122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;

Query Match   62.3%; Score 429.5; DB 1; Length 122;
Best Local Similarity   67.7%; Pred. No. 7.3e-36;
Matches 84; Conservative 14; Mismatches 19; Indels 7; Gaps 2;

Qy   9 VESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNTYIYYADAV 68
           |||||||:||| |||||||||||||||:|||||||||||||||:||||::||
Db   5 VESGGGVVZPGRSLRLSCAASGFTFSNYAMHWVRQPPGKGLEWVAVISYBGBBKYYABSV 64

Qy   69 KGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARD-SRYSNFLRWVRSDGMDVWGQGTTV 127
           |||||||||:||||::|| ||||| |:|| ||| |:
Db   65 KGRFTISRDBSKBTLLYLQMNSLRAEBTAVYYCARDRPLYGBY-----RAFNYWGQGTLV 118

Qy   128 IVSS 131
           |:||
Db   119 TVSS 122

RESULT 3
ID   HV3B_HUMAN   STANDARD;   PRT;   114 AA.
AC   P01763;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-III region WEA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=83273707; PubMed=6410398;
RA   Goni F., Frangione B.;
RT   "Amino acid sequence of the Fv region of a human monoclonal IgM
RT   (protein WEA) with antibody activity against 3,4-pyruvylated
RT   galactose in Klebsiella polysaccharides K30 and K33.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC   AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC   WALDENSTROM'S MACROGLOBULINEMIA.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02046; M3HUWE.
HSSP; P01772; 2PB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
DOMAIN   1   112   IG-LIKE.
MOD_RES   1   1   PYRROLIDONE CARBOXYLIC ACID.
NON_TER   114   114
SQ   SEQUENCE   114 AA; 12256 MW; D88294FB418A07B7 CRC64;

Query Match   61.6%; Score 424.5; DB 1; Length 114;
Best Local Similarity   65.6%; Pred. No. 2.1e-35;
Matches 86; Conservative 15; Mismatches 13; Indels 17; Gaps 3;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
           :||| |||||||||||||||||||||||||||:|||||||||||||||:
Db   1 QVQL----VDSGGGLVEPGGSLRLSCAASGFTFSANDMNWVRQAPGKGLEWLSFIGGSGS 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
           :||||:||||||||||||:||||||||:||||||||||||||:
Db   57 TIYYADSVKGRFTISRNBSKNSLYLQMSSLRAEDTAVYYCARG------WLLN---- 103

Qy   121 WGQGTTVIVSS 131
           ||||||:|||
Db   104 WGQGTLVTVSS 114

RESULT 4
ID   HV3C_HUMAN   STANDARD;   PRT;   117 AA.
AC   P01764;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-III region VH26 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]

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       SEQUENCE FROM N.A.
RP
RX     MEDLINE=81101090; PubMed=6450418;
RA     Matthyssens G., Rabbitts T.H.;
RT     "Structure and multiplicity of genes for the human immunoglobulin
RT     heavy chain variable region.";
RL     Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
CC     -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
```

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DR     EMBL; J00236; AAA53516.1; -.
DR     EMBL; M35415; AAA58735.1; -.
DR     PIR; A02047; H3HU26.
DR     PDB; 1HOU; 23-DEC-99.
DR     Genew; HGNC:5545; IGHV3.
DR     GO; GO:0005576; C:extracellular; NAS.
DR     GO; GO:0003823; F:antigen binding activity; NAS.
DR     GO; GO:0006955; P:immune response; NAS.
DR     InterPro; IPR007110; Ig-like.
DR     InterPro; IPR003006; Ig_MHC.
DR     InterPro; IPR003596; Ig_V.
DR     Pfam; PF00047; ig; 1.
DR     SMART; SM00406; IGv; 1.
DR     PROSITE; PS50835; IG_LIKE; 1.
KW     Immunoglobulin V region; Signal; 3D-structure.
FT     SIGNAL        1     19
FT     CHAIN        20    117       IG HEAVY CHAIN V-III REGION VH26.
FT     DOMAIN       20    117       IG-LIKE.
FT     NON_TER     117    117
SQ     SEQUENCE   117 AA;  12582 MW;  E82673F1A3C0F1 CRC64;

Query Match             60.8%;  Score 419;  DB 1;  Length 117;
Best Local Similarity   80.4%;  Pred. No. 7.7e-35;
Matches    82; Conservative    7; Mismatches    9; Indels    4; Gaps    1;

Qy    1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
          ||||| :|  || |||||||||||||||||||||||||| |||  ||||||||||||||
Db   20 EVQLL----ESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGG 75

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCAR 102
          ||||||||||||||||||| ||| |||||||||| ||||||
Db   76 STYYGDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK 117
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RESULT 5
ID   HV3H_HUMAN     STANDARD;     PRT;   122 AA.
AC   P01769;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-III region GA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=74175307; PubMed=4208843;
RA   Florent G., Lehman D., Putnam F.W.;
RT   "The switch point in mu heavy chains of human IgM immunoglobulins.";
RL   Biochemistry 13:2482-2498(1974).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC       MACROGLOBULIN.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A02052; M3HUGA.
DR   HSSP; P01772; 2FB4.
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DR     GO; GO:0005576; C:extracellular; NAS.
DR     GO; GO:0003823; F:antigen binding activity; NAS.
DR     GO; GO:0006955; P:immune response; NAS.
DR     InterPro; IPR007110; Ig-like.
DR     InterPro; IPR003006; Ig_MHC.
DR     InterPro; IPR003596; Ig_V.
DR     Pfam; PF00047; ig; 1.
DR     SMART; SM00406; IGv; 1.
DR     PROSITE; PS50835; IG_LIKE; 1.
KW     Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT     DOMAIN        1    112       IG-LIKE.
FT     MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT     NON_TER     122    122
SQ     SEQUENCE   122 AA;  13166 MW;  74E5B6959E84100A CRC64;

Query Match             59.1%;  Score 407.5;  DB 1;  Length 122;
Best Local Similarity   59.5%;  Pred. No. 1.1e-33;
Matches    78; Conservative    21; Mismatches    23; Indels    9; Gaps    2;

Qy    1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
          :|:|   ||||||||||||||||||||||||| ||||||||||||||||| ||:
Db    1 QVZL---VZSGGGAVZPGRSLRLSCAASGFSFSTYAMHWVRQAPGKGLEWVSS 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCAR--------SG 102
          ||||| ||||||||||  : | ||| |||||||| |||||||      ||
Db   57 BZTYAASVKGRFTISRBBSKBTMYLEMNSLRAENTAVYYCARSG-----IALGSVAGTDY 111

Qy  103 WGQGTTVVSS 131
          ||  || :||
Db  112 WG2GTLVTISS 122
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RESULT 6
ID   HV3K_HUMAN     STANDARD;     PRT;   126 AA.
AC   P01772;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-III region KOL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE, AND DISULFIDE BONDS.
RX   MEDLINE=83289131; PubMed=6884994;
RA   Marquart M., Deisenhofer J., Huber R., Palm W.;
RT   "Crystallographic refinement and atomic models of the intact
RT   immunoglobulin molecule Kol and its antigen-binding fragment at 3.0 A
RT   and 1.0-A resolution.";
RL   J. Mol. Biol. 141:369-391(1980).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX   MEDLINE=81072295; PubMed=7417755;
RA   Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT   "Three-dimensional structure determination of antibodies. Primary
RT   structure of crystallized monoclonal immunoglobulin IgG1 KOL. I.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A02055; G1HUKL.
DR   PDB; 2IG2; 12-JUL-89.
DR   PDB; 2FB4; 12-JUL-89.
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FT   DOMAIN        1    112       IG-LIKE.
FT   MOD_RES       1      1       PYROLIDONE CARBOXYLIC ACID.
FT   DISULFID     22     96
FT   DISULFID    105    110
FT   STRAND        3      7
FT   STRAND       11     12
FT   TURN         14     15
FT   TURN         14     15
FT   STRAND       18     25
FT   STRAND       29     31
FT   HELIX        34     39
FT   STRAND       41     42
FT   TURN         41     42
FT   STRAND       53     54
FT   TURN         58     60
FT   HELIX        62     64
FT   STRAND       65     65
FT   STRAND       68     73
FT   TURN         74     77
FT   TURN         78     83
FT   HELIX        88     90
FT   STRAND       92     99
FT   STRAND      106    106
FT   TURN        107    108
FT   TURN        107    108
FT   STRAND      109    109
FT   STRAND      113    116
FT   STRAND      120    124
FT   NON_TER     126    126
FT   NON_TER     126    126
SQ   SEQUENCE    126 AA;  13718 MW;  E4D71B52B16F8776 CRC64;

Query Match             59.1%;  Score 407.5;  DB 1;  Length 126;
Best Local Similarity   62.6%;
Matches   82;  Conservative  18;  Mismatches  26;  Indels   5;  Gaps   2;

Qy    1 EVQLLESGVEGSGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
         |:||| ||||:|||:|||: |||||||||||||||||||||:||||||||||||||::::
Db    1 QVQL----VESGGGVVQPGRSLRLSCSSSGFIFSSTAMYWVRQAPGKGLEWVAIWDDGS 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
         :||:||||||||||||||||:|:||||:|||:| |||| ||||::||: ||
Db   57 DQHYADSVKGRFTISRDNSKNTLFLQMDSLRPEDTGVYFCARDGGH-GFCSSASCFGPDY 115

Qy  121 WGQGTTVIVSS 131
         |||:| | |||
Db  116 WGQGTPVIVSS 126
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DR   GO; GO:0003823; F:antigen binding activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Pyrolidone carboxylic acid.
FT   DOMAIN        1    108
FT   MOD_RES       1      1       PYROLIDONE CARBOXYLIC ACID.
FT   NON_TER     122    122
SQ   SEQUENCE    122 AA;  13472 MW;  2E21A11DA04D80F9 CRC64;

Query Match             59.0%;  Score 406.5;  DB 1;  Length 122;
Best Local Similarity   58.6%;
Matches   78;  Conservative  19;  Mismatches  23;  Indels  13;  Gaps   3;

Qy    1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
         |:||| :||:||||||:||||||||||: |||:||:|: |||||:||||||:|
Db    1 QVQL----VQSGGGLVRPGGSLRLSCVASGFSFRDFIMSWIRZTPGKGLZWVSYIGGSGS 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCA--RDSRYSNFLRWVRSDGM 118
         :||:||:|||||||||||||:|:||||:|||::||||||||||  :
Db   57 TLYADSVKGRFTISRDNAQKSLYLZMBSLRRTZBTAVYYCAATBBFBWSTF------SL 109

Qy  119 DVWGQGTTVIVSS 131
         | ||:| | |||
Db  110 BYWGZGBLVTVSS 122
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RESULT 7
ID   HV3A_HUMAN    STANDARD;    PRT;   122 AA.
AC   P01762;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-III region TRO.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE (MYELOMA PROTEIN TRO).
RX   MEDLINE=76023781; PubMed=809331;
RA   Kratzin H., Altevogt P., Ruban E., Kortt A., Staroscik K.,
RA   Hilschmann N.;
RT   "The primary structure of a monoclonal IgA-immunoglobulin (IgA, Tro),
RT   II. The amino acid sequence of the H-chain, alpha-type, subgroup III;
RT   structure of the complete IgA-molecule.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).
CC   -!- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS ALSO GIVEN.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A02045; A1HUTR.
DR   HSSP; P01772; 2FB4.
DR   GO; GO:0005576; C:extracellular; NAS.
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RESULT 8
ID   HV3J_HUMAN    STANDARD;    PRT;   121 AA.
AC   P01771;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-III region HIL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=79124695; PubMed=420800;
RA   Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
RT   "Amino acid sequence of the VH region of human myeloma
RT   cryoimmunoglobulin IgG Hil.";
RL   Biochemistry 18:553-560(1979).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC       PROTEIN.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A02054; G1HUHL.
DR   HSSP; P01772; 2FB4.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Pyrolidone carboxylic acid.
FT   DOMAIN        1    112       IG-LIKE.
FT   MOD_RES       1      1       PYROLIDONE CARBOXYLIC ACID.
FT   NON_TER     121    121
SQ   SEQUENCE    121 AA;  13566 MW;  480FC53610EF5DAB CRC64;

Query Match             58.6%;  Score 404;  DB 1;  Length 121;
Best Local Similarity   62.6%;
Matches   77;  Conservative  15;  Mismatches  25;  Indels   6;  Gaps   1;
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Qy     9 VESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNTYIYYADAV 68
         |::||:|:|| |||||||||:||||||:|:|| |||||:|||||||||: :    :  :|
Db     5 VQAGGGVQPGRSLRLSCIASGFTFSNYGMHWVRQAPGKGLEWVAVIWYNGSRTYYYGDSV 64

Qy    69 KGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDVWGQGTTVI 128
         ||||||||||:|::|||:||||:|:||||||||||   :    |  :|  ||||| ||:
Db    65 KGRFTISRDNSKRTLYMZMNSLRTEDTAVYYCARDPDI-----LTAFSFDVWGQGVLVT 118

Qy   129 VSS 131
         |||
Db   119 VSS 121
```

RESULT 9
HV3E_HUMAN

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ID   HV3E_HUMAN     STANDARD;      PRT;   120 AA.
AC   P01766;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-III region BRO.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=77117674; PubMed=65324;
RA   Capra J.D., Hopper J.E.;
RT   "Comparative studies on monotypic IgM lambda and IgG kappa from an
RT   individual patient III. The complete amino acid sequence of the VH
RT   region of the IgM paraprotein.";
RL   Immunochemistry 13:995-999(1976).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGM ISOLATED FROM THE
CC       SERUM OF A PATIENT WITH MALIGNANT LYMPHOMA OF THE WALDENSTROM
CC       TYPE.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A02049; M3HUBW.
DR   HSSP; P01772; 2FB4.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1    111       IG-LIKE.
FT   NON_TER       1      1
FT   NON_TER     120    120
SQ   SEQUENCE   120 AA;  13227 MW;  D3F0428F7C2E6410 CRC64;

Query Match             58.3%;  Score 402;  DB 1;  Length 120;
Best Local Similarity   68.8%;  Pred. No. 3.8e-33;
  Matches   86;  Conservative   11;  Mismatches   22;  Indels    6;  Gaps    3;

Qy     1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
         |||| ||:||||||||||||||||||||||||||||||:|||||||||||||| :||||:
Db     1 EVQL----VESGGGLVQPGGSLRLSCAASGFTFSYYNMNWVRQVTGKGLEWVSAIGTAGD 56

Qy    61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
         |||:||||||||||||:|||||| |||||||||||||||||||:  :.:|||||||| |
Db    57 Q-YYADSVKGRFTISRDNSKNTLYLNMNSLRAEDTAVYYCAR-SPVSLVDGWLYYYGSV 114

Qy   121 WGQGT 125
         |||||
Db   115 WGQGT 119
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ID   HV3F_HUMAN     STANDARD;      PRT;   115 AA.
AC   P01767;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-III region BUT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=78137069; PubMed=416441;
RA   Torano A., Putnam F.W.;
RT   "Complete amino acid sequence of the alpha 2 heavy chain of a human
RT   IgA2 immunoglobulin of the A2m(2) allotype.";
RL   Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
CC   -!- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE, C
CC       REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A02050; A2HUBU.
DR   HSSP; P01789; 1MCP.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1    111       IG-LIKE.
FT   NON_TER       1      1
FT   NON_TER     115    115
SQ   SEQUENCE   115 AA;  12379 MW;  208876A7DF52DCF4 CRC64;

Query Match             58.1%;  Score 400;  DB 1;  Length 115;
Best Local Similarity   61.8%;  Pred. No. 5.8e-33;
  Matches   81;  Conservative   18;  Mismatches   16;  Indels   16;  Gaps    3;

Qy     1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
         |||| ||:| |:|||||:|||||||||||||||||||:|||||| |:||||||| :|
Db     1 EVQL----VETGGGLIQPGGSLRLSCAASGFTFSYYNMNWVRQVTGKGLEWVSAIYRGGT 56

Qy    61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
         |||:||||||||||||:  |: ::|||:|||||||||||||||:
Db    57 -TYYADSVKGRFTISRDDSRBTVILQMBSLRAEDTAVYYCARDLAAAR-----------L 104

Qy   121 WGQGTTVIVSS 131
         :||||||:|||
Db   105 FGKGTTVTVSS 115
```

RESULT 11
HV3T_HUMAN

```
ID   HV3T_HUMAN     STANDARD;      PRT;   116 AA.
AC   P01781;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-III region GAL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=75059123; PubMed=4803843;
RA   Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
RT   "The primary structure of a monoclonal IgM-immunoglobulin
RT   (macroglobulin Gal.), II: the amino acid sequence of the complete H-chain (mu-
RT   type), subgroup H III. Architecture of the complete IgM-molecule.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
```

RESULT 10
HV3F_HUMAN

```
RN   [2]
RP   REVISION TO 28-33.
RA   Hilschmann N.;
RL   Submitted (JUN-1975) to the PIR data bank.
CC   -!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC       MACROGLOBULIN.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A02064; M3HGL.
DR   HSSP; P01772; 2FB4.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig-v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN    1      112
FT   NON_TER   116    116
SQ   SEQUENCE   116 AA;  12730 MW;  2C67CA9AAAA1282 CRC64;

Query Match
Best Local Similarity   57.7%;
Matches  84; Conservative  7; Mismatches  25; Indels  15; Gaps  3;

Qy    1  EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWHWVRQGPGKGLEWVSSISNSNT   60
         ||||||||||||||||||||:||:|||||||||||||||:||||:||::||::|::::::
Db    1  EVQL---VESGGDLVQPGRSLRLSCAASGFBFBBLGMTWVRQAPGKGLEWVANIKZBGS    56

Qy   61  YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV  120
         |:||||||||||||||||||||||||:||:||||:|:|:||||  :|||:|:||||
Db   57  ZZBYVDSVKGRFFISRDNAKNSLIYLQMNSLRVEDTALYYCARG------W---GGGDY  105

Qy  121  WGGGTTVIVSS 131
         ||||| |  |:
Db  106  WGQGTLVTVST 116


RESULT 12
ID   HV57_MOUSE    STANDARD;    PRT;   98  AA.
AC   P18528;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain v region 6.96.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89279149; PubMed=2499654;
RA   Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT   "Early onset of somatic mutation in immunoglobulin VH genes during
RT   the primary immune response.";
RL   J. Exp. Med. 169:2007-2019(1989).
CC   -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; JT0501; HVMS96.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig-v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN    1      >98     IG-LIKE.
FT   NON_TER   98     98
```

```
SQ   SEQUENCE   98 AA;   11007 MW;  B8644E7F92FBF95B CRC64;

Query Match
Best Local Similarity   57.3%;    Score 395;  DB 1;  Length 98;
Matches  76; Conservative  12; Mismatches  10; Indels  4; Gaps  1;

Qy    1  EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWHWVRQGPGKGLEWVSSISNSNT   60
         ||||| :||||||||||:|:||||:|||||||||||:|:|:||||||:||||::|:: :
Db    1  EVQL---VESGGGLVKPGGSLKLSCAASGFTFSDYMYWVRQRTPEKRLEWVATISDGGS    56

Qy   61  YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCAR 102
         ||||||||||||||||||||||:||:||:||:||:|| ||
Db   57  YTYYPDSVKGRFTISRDNAKNNLYLQMNSLKSEDTAMYYCAR  98


RESULT 13
ID   HV38_MOUSE    STANDARD;    PRT;   119 AA.
AC   P01808;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain v region T601.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=79223895; PubMed=111245;
RA   Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
RT   "Structural evidence for independent joining region gene in
RT   immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT   its potential role in generating diversity in
RT   complementarity-determining regions.";
RL   Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
CC       THAT BINDS GALACTAN.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A02078; AVMST6.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig-v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN    1      112     IG-LIKE.
FT   NON_TER   119    119
SQ   SEQUENCE   119 AA;  13169 MW;  BC38CC84E66BA00E8 CRC64;
```

```
Query Match
Best Local Similarity   56.8%;    Score 391.5;  DB 1;  Length 119;
Matches  79; Conservative  15; Mismatches  24; Indels  13; Gaps  2;

Qy    1  EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWHWVRQGPGKGLEWVSSISNSNT   60
         ||||| :|| :|||||||:||||:|||||||||||||:|:|:||||||:|||| :
Db    1  EVKLL---ESGGGLVQPGGSLKLSCAASGFDFSRVWMSWVRQAPGKGLEWIGEINPDSS    56

Qy   61  YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV  120
         |::||| :|:|||||||||||:|:|||||||||||| :|||| :|||:|:||||
Db   57  TINTTPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCARLGYYGYF-------DV  107

Qy  121  WGQGTTVIVSS 131
         ||| |||| |||
Db  108  WGAGTTVTVSS 118


RESULT 14
ID   HV3I_HUMAN    STANDARD;    PRT;   119 AA.
AC   P01770;
```

```
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-III region NIE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=77070269; PubMed=826475;
RA   Ponstingl H., Hilschmann N.;
RT   "The rule of antibody structure. The primary structure of a
RT   monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The
RT   chymotryptic peptides of the H-chain, alignment of the tryptic
RT   peptides and discussion of the complete structure.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN   [2]
RP   DISULFIDE BOND.
RX   MEDLINE=77070267; PubMed=1002129;
RA   Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
RT   characterization of the protein, the L- and H-chains, the
RT   cyanogen bromide cleavage products, and the disulfide bridges.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC       PROTEIN.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A91668; GIHUNI.
DR   HSSP; P01772; 2FB4.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT   DOMAIN        1    112       IG-LIKE.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     22     96
FT   NON_TER     119    119
SQ   SEQUENCE   119 AA;  13242 MW;  C9693SA6E55E165B CRC64;

Query Match             56.7%;  Score 391;  DB 1;  Length 119;
Best Local Similarity   60.9%;  Pred. No. 4.7e-32;
Matches   81;  Conservative  15;  Mismatches  21;  Indels  16;  Gaps  3;

Qy     1 EVQLLESGVESGGGGLVKPGGSLRLSCAAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
           :|||:|:|:|||||:||  ||||||||||||||||||||||:||||||||||||||  ||
Db     1 QVQL----VQSGGGVVQPGRSLRLSCAASGFTFSRYTIHWVRQAPGKGLEWVAVMSYEGB 56

Qy    61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
          ||||:||||||||||||||||||||||:|||| ||||||||||  ||||||||
Db    57 BKHYADSVNGRFTISRNDSKNTLYLNMNSLRPEDTAVYYCAR---------IRDTAMFF 106

Qy   121 --WGQGTTVTVSS 131
           |||||  |||
Db   107 AHWGQGTLVTVSS 119
```

```
RESULT 15
ID   HV02_CANFA     STANDARD;      PRT;   117 AA.
AC   P01785;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region MOO.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE OF 1-112.
RX   MEDLINE=77242268; PubMed=407924;
RA   Wasserman R.L., Capra J.D.;
RT   "Primary structure of the variable regions of two canine
RT   immunoglobulin heavy chains.";
RL   Biochemistry 16:3160-3168(1977).
RN   [2]
RP   SEQUENCE OF 113-117.
RX   MEDLINE=80077682; PubMed=117299;
RA   McCumber L.J., Capra J.D.;
RT   "The complete amino-acid sequence of a canine mu chain.";
RL   Mol. Immunol. 16:565-570(1979).
CC   -!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A90403; MHDGMO.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1    116       IG-LIKE.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12703 MW;  FCE07309E0A84B35 CRC64;

Query Match             56.6%;  Score 390;  DB 1;  Length 117;
Best Local Similarity   62.5%;  Pred. No. 5.8e-32;
Matches   85;  Conservative   9;  Mismatches  18;  Indels  24;  Gaps  4;

Qy     1 EVQLLESGVESGGGGLVKPGGSLRLSCAAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
          |:|    ||||:||||||||||||:|||||||||:|||| :|:|::: |::|:|:|:|:|
Db     1 EVKL----VESGGDLVKPGGSLRLSCVASGFTFSSNGMSWVRQDPGEGLQWVADISSSG- 55

Qy    61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDS-----RYSNFLRWVRS 115
          ||||||||||||:|||||||||:||||:||::||| ||||| | ||  |||  |||||
Db    56 QTYYADAVKGRFSISRDNAKNTLYLQMEDLRVEDTAVYYCATEGDIEIPRY-------- 106

Qy   116 DGMDVWGQGTTVTVSS 131
          :|||:||||| |||
Db   107 ----FGQGTIVTVSS 117
```

Search completed: September 24, 2003, 06:27:32
Job time : 34 secs

```
                    GenCore version 5.1.6
                    Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:       September 24, 2003, 05:40:25 ; Search time 75 Seconds
                                            (without alignments)
                                            450.732 Million cell updates/sec

Title:            US-09-848-798A-28
Perfect score:    689
Sequence:         1 EVQLLESGVESGGGLVKPGG........WVRSDGMDVWGQGTTVIVSS 131

Scoring table:    BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched:         830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters:       830525

Post-processing: Minimum Match 0%
                 Maximum Match 100%
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                 Listing first 45 summaries

Database :   SPTREMBL_23:*
         1:  sp_archea:*
         2:  sp_bacteria:*
         3:  sp_fungi:*
         4:  sp_human:*
         5:  sp_invertebrate:*
         6:  sp_mammal:*
         7:  sp_mhc:*
         8:  sp_organelle:*
         9:  sp_phage:*
        10:  sp_plant:*
        11:  sp_rodent:*
        12:  sp_virus:*
        13:  sp_vertebrate:*
        14:  sp_unclassified:*
        15:  sp_rvirus:*
        16:  sp_bacterial:*
        17:  sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	%Query Match	Length	DB	ID	Description
1	500.5	72.6	471	4	Q8TC77	Q8tc77 homo sapien
2	477.5	69.3	118	4	Q9UL91	Q9ul91 homo sapien
3	466.5	67.7	494	4	Q96K68	Q96k68 homo sapien
4	463	67.2	597	4	Q96BB9	Q96bb9 homo sapien
5	461.5	67.0	573	4	Q8WU38	Q8wu38 homo sapien
6	455.5	66.1	613	4	Q8WUK1	Q8wuk1 homo sapien
7	453.5	65.8	473	11	Q91ZO5	Q91zo5 mus musculu
8	453	65.7	113	4	Q9UL90	Q9ul90 homo sapien
9	450	65.3	121	4	Q9UL71	Q9ul71 homo sapien
10	445.5	64.7	487	11	Q99KA4	Q99ka4 mus musculu
11	432	62.7	116	4	Q9UL93	Q9ul93 homo sapien
12	430	62.4	499	4	Q8N5K4	Q8n5k4 homo sapien
13	427.5	62.0	112	4	Q9HCC1	Q9hcc1 homo sapien
14	426.5	61.9	122	4	Q9UL84	Q9ul84 homo sapien
15	426	61.8	119	11	Q920E7	Q920e7 mus musculu
16	423.5	61.5	118	4	Q9UL72	Q9ul72 homo sapien
17	423.5	61.5	147	4	Q9Y509	Q9y509 homo sapien
18	413	59.9	493	11	Q8NCL6	Q8nc16 homo sapien
19	401	58.2	479	11	Q91WP5	Q91wp5 mus musculu
20	384	57.3	95	4	Q9ULB6	Q9ulb6 homo sapien
21	381.5	55.7	480	11	Q91XE1	Q91xe1 mus musculu
22	381.5	55.4	469	11	Q8R3V9	Q8r3v9 mus musculu
23	376	54.6	486	11	Q91Z07	Q91z07 mus musculu
24	373.5	54.2	298	11	Q9QYF0	Q9qyf0 mus musculu
25	369.5	53.6	484	11	Q8VEA0	Q8vea0 mus musculu
26	365.5	53.0	131	11	Q9UL88	Q9ul88 mus musculu
27	365.5	53.0	437	11	Q9R1A4	Q91a4 mus musculu
28	362	52.5	104	4	Q9UL87	Q9ul87 homo sapien
29	357	51.8	521	4	Q8N4Y9	Q8n4y9 homo sapien
30	349.5	50.7	124	6	Q9N0W4	Q9n0w4 oryctolagus
31	347	50.4	112	4	Q9UGP3	Q9ugp3 homo sapien
32	346.5	50.3	124	6	Q9N0W6	Q9n0w6 oryctolagus
33	336.5	48.8	124	4	Q9UL92	Q9l92 homo sapien
34	325	47.2	125	4	Q9UL95	Q9ul95 homo sapien
35	320.5	46.5	159	4	Q96QS0	Q96qs0 homo sapien
36	319	46.3	142	11	Q924Q1	Q924q1 mus musculu
37	317	46.0	117	11	Q9QXE9	Q9qxe9 mus musculu
38	315.5	45.8	109	11	Q9JL75	Q9jl75 mus musculu
39	315.5	45.8	482	11	Q8K172	Q8k172 mus musculu
40	314.5	45.6	143	11	Q91VA2	Q91va2 mus musculu
41	314.5	45.6	143	11	Q924R7	Q924r7 mus musculu
42	313	45.4	484	11	Q91A6	Q91a6 mus musculu
43	311.5	45.2	143	11	Q924R0	Q924r0 mus musculu
44	311	45.1	117	11	Q9XF0	Q9xf0 mus musculu
45	311	45.1	142	11	Q924Q2	Q924q2 mus musculu

ALIGNMENTS

```
RESULT 1
Q8TC77

Q8TC77        PRELIMINARY;        PRT;        471 AA.
ID   Q8TC77;
AC   Q8TC77;
DT   01-JUN-2002 (TREMBLrel. 21, Created)
DT   01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT   01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC024289; AAH24289.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE 471 AA;   388F7F4CF58B660E CRC64;

DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.

Query Match             72.6%;  Score 500.5;  DB 4;   Length 471;
Best Local Similarity   77.9%;  Pred. No. 5.6e-41;
Matches  102;  Conservative   8;  Mismatches  12;  Indels  9;  Gaps   3;

Qy     1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
         |||| |||||||||||||||||||||||||||||||||||||||||||||:|:|||||
Db    20 EVQL---VESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSMSSSSS 75

Qy    61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
         |||||:||||||||||||||||||||||||||||||||||||||| |:
Db    76 YIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLRQLTSY-WY----FDL 130
```

```
Qy  121 WGQGTTVIVSS 131
        |:||| |||
Db  131 WGRGTLVTVSS 141
```

RESULT 2
Q9UL91
```
ID   Q9UL91;      PRELIMINARY;     PRT;    118 AA.
AC   Q9UL91;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=9277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035023; AAD56259.1; -.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig-MHC.
DR   InterPro; IPR003596; Ig-V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER     1      1
FT   NON_TER   118    118
SQ   SEQUENCE   118 AA;  12843 MW;  D0633949F2AC149D CRC64;
```

```
Query Match             69.3%;
Best Local Similarity   75.6%;          Score 477.5;   DB 4;   Length 118;
Matches    99;  Conservative   7;       Pred. No. 1.9e-39;
Mismatches 10;  Indels  15;  Gaps  3;

Qy    1 EVQLLESGVESGGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPCKGLEWVSSISNSNT 60
Db    1 EVQL----VESGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSISSTII 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCAR-DSRYSNFLRWVRSDGMD 119
Db   57 TIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGDS------------SEAFD 106

Qy  120 VWGQGTTVIVS 130
Db  107 IWGQGTMVTVS 117
```

RESULT 3
Q96K68
```
ID   Q96K68;      PRELIMINARY;     PRT;    494 AA.
AC   Q96K68;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein FLJ14473.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wagatsuma M., Hosoiri T., Kaku T., Kodaira H., Kondo H., Sugawara M.,
RA   Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA   Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA   Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA   Ninomiya K., Iwayanagi T.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK027379; BAB55072.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig-MHC.
DR   InterPro; IPR003596; Ig-V.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   494 AA;  53088 MW;  9A1D7AEB5AEE4C0E CRC64;
```

```
Query Match             67.7%;          Score 466.5;   DB 4;   Length 494;
Best Local Similarity   72.5%;          Pred. No. 1.3e-37;
Matches    95;  Conservative   8;  Mismatches  19;  Indels   9;  Gaps  2;

Qy    1 EVQLLESGVESGGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPCKGLEWVSSISNSNT 60
Db   20 EVQL----VESGGGLVKPGGSLRLSCAASGLSFSTYAMNWVRQAPGKGLEWVSISSRSD 75

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
Db   76 YIYYRDSVKGRFTISRDNAKNSLYLQMNSLRVDDTAVYYCARDS-----CNGAICYGFSP 130

Qy  121 WGQGTTVIVSS 131
Db  131 WGQGTLVTVSS 141
```

RESULT 4
Q96BB9
```
ID   Q96BB9;      PRELIMINARY;     PRT;    597 AA.
AC   Q96BB9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B-cell;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC015760; AAH15760.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig-MHC.
DR   InterPro; IPR003596; Ig-V.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE   597 AA;  65039 MW;  4FCA3AD8ECE263D9 CRC64;
```

```
Query Match             67.2%;          Score 463;   DB 4;   Length 597;
Best Local Similarity   72.0%;          Pred. No. 3.7e-37;
Matches    95;  Conservative  12;  Mismatches  17;  Indels   8;  Gaps  3;

Qy    1 EVQLLESGVESGGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPCKGLEWVSSISNSNT 60
Db   20 EVQL----ESGGGLVQPGGSLRLSCAASGFSSYAMNWVRQAPGKGLEWVSAISGSGG 75

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSR-YSNFLRWVRSDGMD 119
```

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Db      76 STYYADSVKGRFPISRDNSRDTLYLQMNSLRAEDTAVYYCAKDPRGYSASGNYTRE---D 132

Qy     120 VWGQGTLVTVSS 131
           ||| ||||
Db     133 YWGQGTLVTVSS 144
```

```
RESULT 5
Q8WU38
ID      Q8WU38;             PRELIMINARY;      PRT;     573 AA.
AC      Q8WU38;
DT      01-MAR-2002 (TrEMBLrel. 20, Created)
DT      01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT      01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE      Hypothetical protein.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Tonsil;
RA      Strausberg R.;
RL      Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; BC021276; AAH21276.1; -.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF00047; ig; 4.
DR      SMART; SM00406; IGv; 1.
DR      PROSITE; PS50835; IG_LIKE; 2.
DR      PROSITE; PS00290; IG_MHC; 2.
KW      Hypothetical protein.
SQ      SEQUENCE   573 AA;  62967 MW;  FD072344033AC530 CRC64;
```

```
Query Match              67.0%;   Score 461.5;  DB 4;  Length 573;
Best Local Similarity    73.3%;   Pred. No. 4.9e-37;
Matches   96;  Conservative   8;  Mismatches  20;  Indels   7;  Gaps   2;
```

```
Qy       1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
           ||||   |:|||||||||||||||||||| ||||||||||||||||||| || ::
Db      20 EVQL---VESGGGLVQPGRSLRLSCAASGFTFDDYAMHVRQAPGKGLEWVSGISWNSG 75

Qy      61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
           | |:|::||||||||||||||||||| | |||||:
Db      76 SIGYADSVKGRFTISRDNAKNSLYLRAEDTALYYCAKHGSGSSYIGYY---GMDV 132

Qy     121 WGQGTTVIVSS 131
           |||||| ||
Db     133 WGQGTTVIVSS 143
```

```
RESULT 6
Q8WUK1
ID      Q8WUK1;             PRELIMINARY;      PRT;     613 AA.
AC      Q8WUK1;
DT      01-MAR-2002 (TrEMBLrel. 20, Created)
DT      01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT      01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE      Hypothetical protein.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Tonsil;
RA      Strausberg R.;
RL      Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; BC020240; AAH20240.1; -.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF00047; ig; 5.
DR      SMART; SM00406; IGv; 1.
DR      PROSITE; PS50835; IG_LIKE; 5.
DR      PROSITE; PS00290; IG_MHC; 3.
KW      Hypothetical protein.
SQ      SEQUENCE   613 AA;  67296 MW;  60C7F59506071E3315 CRC64;
```

```
Query Match              66.1%;   Score 455.5;  DB 4;  Length 613;
Best Local Similarity    69.4%;   Pred. No. 2.1e-36;
Matches   93;  Conservative  12;  Mismatches  12;  Indels  17;  Gaps   4;
```

```
Qy       1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
           ||||   |:||||||||||||||||||||||||||||||||||||:  | ::
Db      20 QVQL----VESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGS 75

Qy      61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGM-- 118
           | |:|::||||||||||||||:||:||:||:||||||||||| |||||||||||:  | :
Db      76 NKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKD------W--SECVET 125

Qy     119 -DVWGQGTTVTVSS 131
           :|||||||| |||
Db     126 FDIWGQGTMVTVSS 139
```

```
RESULT 7
Q91Z05
ID      Q91Z05;             PRELIMINARY;      PRT;     473 AA.
AC      Q91Z05;
DT      01-DEC-2001 (TrEMBLrel. 19, Created)
DT      01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT      01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE      Hypothetical 51.9 kDa protein.
OS      Mus musculus (Mouse).
GN      AU044919.
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Strausberg R.;
RL      Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; BC010327; AAH10327.1; -.
DR      MGD; MGI:2144967; AU044919.
DR      InterPro; IPR000345; Cytc_heme_bind.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF00047; ig; 3.
DR      SMART; SM00406; IGv; 1.
DR      PROSITE; PS00190; CYTOCHROME_C; 1.
DR      PROSITE; PS50835; IG_LIKE; 4.
DR      PROSITE; PS00290; IG_MHC; 1.
KW      Hypothetical protein.
SQ      SEQUENCE   473 AA;  51946 MW;  CF625F008932AF12 CRC64;
```

```
Query Match              65.8%;   Score 453.5;  DB 11;  Length 473;
Best Local Similarity    68.8%;   Pred. No. 2.4e-36;
Matches   90;  Conservative  13;  Mismatches  15;  Indels  13;  Gaps   3;
```

```
Qy       1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
           ||||   |:|||||||||||||||||||||||||||||||||||||:  | ::
Db      20 EVQL----VESGGGLVKPGGSRKLSCAASGFTFSDYGMHWVRQAPEKGLEWVAVISGST 75

Qy      61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
           | |:|::||||||||||||||:||:||:||:||||||||||| ::: ||||||||||
Db      76 TIYYADTVKGRFTISRDNAKNTLFLQMTSLRSEDTAMYYCARE------LWLRR--IDY 126

Qy     121 WGQGTTVTVSS 131
           ||||||: ||
Db     127 WGQGTITVSS 137
```

```
RESULT 8
```

Q9UL90
```
ID   Q9UL90;      PRELIMINARY;   PRT;   113 AA.
AC   Q9UL90;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035024; AAD56260.1; -.
DR   HSSP; P01772; 2FB4.
DR   Pfam; PF00047; ig; 1.
DR   InterPro; IPR003596; Ig_v.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR007110; Ig-like.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER        1      1
FT   NON_TER      113    113
SQ   SEQUENCE   113 AA;  12437 MW;  ED57FDD19086D07F CRC64;

Query Match    Best Local Similarity   65.78%;   Score 453;  DB 4;  Length 113;
               Conservative  69.5%;   Pred. No. 4.6e-37;
Matches  91;   Conservative  8;   Mismatches  14;   Indels  18;   Gaps  2;

Qy    1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT  60
        |||| :|||||| || ||||||||||||||||||||||||||||||||||||| :
Db    1 EVQL----VESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIRYDGS  56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
        :|||| :||||||||||||||: ||||||||||:||||| |:|||| |||
Db   57 NKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDLNY------------ 102

Qy  121 WGQGTTVIVSS 131
        ||||| | |||
Db  103 WGQGTLVTVSS 113
```

RESULT 9
Q9UL71
```
ID   Q9UL71;      PRELIMINARY;   PRT;   121 AA.
AC   Q9UL71;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035043; AAD56279.1; -.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER        1      1
FT   NON_TER      121    121
SQ   SEQUENCE   121 AA;  13154 MW;  2F04SCCFA5D50736 CRC64;

Query Match    Best Local Similarity   65.38%;   Score 450;  DB 4;  Length 121;
               Conservative  68.7%;   Pred. No. 9.9e-37;
Matches  90;   Conservative  10;   Mismatches  21;   Indels  10;   Gaps  2;

Qy    1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT  60
        |||| :||||||   ||||||||| ||||||||| |: |||||||||||||||| :
Db    1 EVQL----VESGGGVVQPGGSLRLFCAASGFTFDGYAMHWVRQAPGKGLEWVSLISGDGG  56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
        :|||| :||||||||||||||: |||||||||||:||||| |: |  | :
Db   57 STYYADSVKGRFTISRDNSKNSLYLQMNSLRAEDTALYYCAKGKVTTIY-----DRFDI 110

Qy  121 WGQGTTVIVSS 131
        ||||| | |||
Db  111 WGQGTMVTVSS 121
```

RESULT 10
Q99KA4
```
ID   Q99KA4;      PRELIMINARY;   PRT;   487 AA.
AC   Q99KA4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical 52.6 kDa protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC004786; AAH04786.1; -.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   487 AA;  52554 MW;  7DC8E9S6DB333077B CRC64;

Query Match    Best Local Similarity   64.7%;   Score 445.5;  DB 11;  Length 487;
               Conservative  67.2%;   Pred. No. 1.5e-35;
Matches  90;   Conservative  14;   Mismatches  17;   Indels  13;   Gaps  3;

Qy    1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT  60
        |||| :|||||||||||||| | |||||||||| |:| |||| |: |||||| :
Db   20 EVQL----VESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTPEKRLEWVATISDGGS  75

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARD--SRYSNFLRWVRSDG 117
        ||||  :|||||||||||||| : ||| :| ||:||:|||||   :  |    : :|
Db   76 YIYYPDNVKGRFTISRDNAKNNIYLQMSHLKSEDTAMYYCARDMGGSPYGGYSRF---- 130

Qy  118 MDVWGQGTTVIVSS 131
        : ||||||| ||||
Db  131 -DYWGQGTTVTVSS 143
```

RESULT 11
Q9UL93

```
ID   Q9UL93            PRELIMINARY;   PRT;  116 AA.
AC   Q9UL93;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=9277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035021; AAD56257.1; -.
DR   HSSP; P01772; 2FB4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
FT   NON_TER    1    1
FT   NON_TER    116  116
SQ   SEQUENCE   116 AA;  12434 MW;  0DA034B154DD6061 CRC64;

Query Match             62.7%;  Score 432;  DB 4;  Length 116;
Best Local Similarity   67.7%;  Pred. No. 5.5e-35;
Matches  88;  Conservative  10;  Mismatches  18;  Indels  14;  Gaps   2;

Qy    2 VQLLESGVESGGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNTY 61
          |||||:|:|:||||||||||||||||||||||||||||||||||||||||:||||||:
Db    1 VQL----VESGGGVQPGRSLRLSCAASGFTPSSYAMHWVRQAPGKGLEWVAVISYDGSN 56

Qy   62 IYIYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDVW 121
          ||||:||||||||||||||||||||||||||||||||||||||:|| | |:|||||| |
Db   57 KYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAMYCAGGGGL-------GLGYW 106

Qy  122 GQGTTVTVSS 131
          |||| | |||
Db  107 GQGTLVTVSS 116
```

```
RESULT 12
ID   Q8N5K4            PRELIMINARY;   PRT;  499 AA.
AC   Q8N5K4;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC032249; AAH32249.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 4.
DR   SMART; SM00407; IgC1; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   499 AA;  53376 MW;  93A5C8958205AF32 CRC64;

Query Match             62.4%;  Score 430;  DB 4;  Length 499;
Best Local Similarity   66.7%;  Pred. No. 5.2e-34;
Matches  92;  Conservative   9;  Mismatches  19;  Indels  18;  Gaps   4;

Qy    1 EVQLLESGVESGGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
          |||| :|:|:||||||||||||||||:|||||||| :|:|||||:||||||||||:||||
Db   20 EVQL----VESGGGVVRPGGSLRLSCATSGFTFDDSGASWVRQAPGKGLEWVSSINWNGG 75

Qy   61 YIYIYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARD-SRYSNFLRWVRSDG-- 117
          | |:|||||||||||||||||||||||||||||:||| |||||  |:|| |:    ||
Db   76 STNYADSVKGRFTISRDNAKNSLYLQMNSLRVEDTALYYCARDPTKYC------SGGSC 128

Qy  118 ----MDVWGQGTTVTVSS 131
          |||:||| :|||||||
Db  129 LGYYMDVWCKGTTVTVSS 146
```

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RESULT 13
ID   Q9HCC1            PRELIMINARY;   PRT;  112 AA.
AC   Q9HCC1;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Single chain Fv (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
RT   "An antibody fragmentA3 specific for native lysozyme :isolaion from a
RT   human synthetic phage display library and characterization.";
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB049915; BAB16829.1; -.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER    1    1
FT   NON_TER    112  112
SQ   SEQUENCE   112 AA;  12243 MW;  24F1A45EC3B4788 CRC64;

Query Match             62.0%;  Score 427.5;  DB 4;  Length 112;
Best Local Similarity   69.3%;  Pred. No. 1.5e-34;
Matches  88;  Conservative   8;  Mismatches  16;  Indels  15;  Gaps   3;

Qy    1 EVQLLESGVESGGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
          ||||| :|:|:|||||||||||||:||||||||| :|:|||||:||||||||| |:
Db    1 EVQL----VESGGGVVRPGGSLRISCAASGFTFDDYGMSWVRQAPGKGLEWVSGINWNGG 56

Qy   61 YIYIYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
          |||:||||||||||||||||||||||||||||:||||||||| |||  |:||     ||
Db   57 STGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR-RRYA-------------LDY 105

Qy  121 WGQGTTV 127
          ||||| |
Db  106 WGQGTLV 112
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RESULT 14
Q9UL84
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ID   Q9UL84            PRELIMINARY;      PRT;   122 AA.
AC   Q9UL84;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=9277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035030; AAD56266.1; -.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  13579 MW;  36054D4136654SB8 CRC64;

Query Match             61.9%;  Score 426.5;  DB 4;  Length 122;
Best Local Similarity   66.9%;  Pred. No. 2e-34;
Matches  89;  Conservative  11;  Mismatches  20;  Indels  13;  Gaps  3;

Qy    1  EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT  60
         ||||  ||| |:||  |||||||||||||||||||||:|||||  |||||||||:||||:
Db    1  EVQL---VESGGGVVQPGRSLRLSCAASRFTFSNYGMHWVRQAPGKGLEWVAAISNDGS  56

Qy   61  YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
         |||:||||||||||||||||||| : ||||:|| |||||||||||:|| |||||||||
Db   57  NKFYADSVKGRFTIFRDNSKNMMDLQMNSLRAEDTAVYYCAKDER------GRLVGTYF 109

Qy  119  DVWGQGTTVIVSS 131
         | ||||||||||
Db  110  DYWGQGTLVTVSS 122
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RESULT 15
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ID   Q920E7            PRELIMINARY;      PRT;   119 AA.
AC   Q920E7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Pterin-mimicking anti-idiotope heavy chain variable region
DE   (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Atkin J.D., Tape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT   "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
RT   in Mammalian Cells.";
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF307937; AAL09421.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     119    119
SQ   SEQUENCE   119 AA;  13025 MW;  F6E90404438ICA7C CRC64;

Query Match             61.8%;  Score 426;  DB 11;  Length 119;
Best Local Similarity   65.6%;  Pred. No. 2.2e-34;
Matches  86;  Conservative  12;  Mismatches  21;  Indels  12;  Gaps  2;

Qy    1  EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT  60
         |||| ||| |:||  |||||||||||||||||||||:|||||  |||||||||:||||: :
Db    1  EVQL---VESGGDLVKPGGSLRLSCAASGFTFSSYGMSWVRQTPDKRLEWVATISSGGS  56

Qy   61  YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
         |||:||||||||||||||||||||:|||||:|| |||||||||:||| |||||||:
Db   57  YTYYPDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARHGDY------DVGFAY 108

Qy  121  WGQGTTVIVSS 131
         |||| ||| |:
Db  109  WGQGTLVTVSA 119

Search completed: September 24, 2003, 06:29:00
Job time : 77 secs
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                                    GenCore version 5.1.6
                            Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:              September 24, 2003, 06:25:35 ; Search time 35 Seconds
                                                    (without alignments)
                                      158.363 Million cell updates/sec

Title:          US-09-848-798A-28
Perfect score:  689
Sequence:       1 EVQLLESGVESGGGLVKPGG.........WVRSDGMDVWGQGTTVIVSS 131

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters:       328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
             1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
             2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
             3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
             4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
             5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
             6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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Result              %      Query
No.    Score   Match  Length  DB   ID                    Description
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  1    689     100.0   131    3    US-09-240-274-28       Sequence 28, Appl
  2    643      93.3   127    3    US-09-240-274-27       Sequence 27, Appl
  3    507.5    73.7   245    4    US-08-918-148-78       Sequence 78, Appl
  4    488      70.8   249    4    US-08-918-148-78       Sequence 53, Appl
  5    481.5    69.9   109    2    US-10-039-785-53       Sequence 53, Appl
  6    481      69.8   123    2    US-08-379-057-32       Sequence 32, Appl
  7    481      69.8   123    4    US-08-665-202-30       Sequence 30, Appl
  8    479.5    69.6   245    4    US-09-315-574-30       Sequence 30, Appl
  9    478.5    69.4   111    1    US-08-211-202-134      Sequence 75, Appl
 10    473.5    68.7   111    1    US-08-918-148-75       Sequence 134, Appl
 11    470.5    68.3   123    1    US-08-211-202-134      Sequence 3, Appl
 12    470.5    68.3   128    1    US-08-478-039-102      Sequence 102, App
 13    470      68.2   128    1    US-08-476-349A-102     Sequence 102, App
 14    470      68.2   117    4    US-09-025-769B-24      Sequence 24, Appl
 15    470      68.2   123    4    US-09-560-198A-2       Sequence 2, Appl
 16    469.5    68.1   128    1    US-08-478-039-73       Sequence 73, Appl
 17    469.5    68.1   128    1    US-08-476-349A-73      Sequence 73, Appl
 18    467.5    67.9   120    4    US-09-025-769B-38      Sequence 38, Appl
 19    467.5    67.9   281    4    US-09-025-769B-178     Sequence 178, Appl
 20    467      67.9   117    4    US-09-025-769B-63      Sequence 63, Appl
 21    463      67.2   117    3    US-08-545-809A-107     Sequence 107, Appl
 22    463      67.2   119    1    US-07-988-925-11       Sequence 11, Appl
 23    463      67.2   119    2    US-08-362-780-11       Sequence 11, Appl
 24    461.5    67.0   127    3    US-09-240-274-139      Sequence 139, App
 25    460      66.8   122    5    PCT-US93-08435-12      Sequence 12, Appl
 26    460      66.8   113    5    US-08-974-899-6        Sequence 6, Appli
 27    458.5    66.5   117    2    US-09-344-587-13       Sequence 13, Appl
 28    458.5    66.5   117    5    US-08-428-197-36       Sequence 36, Appl
 29    458.5    66.5   122    5    PCT-US93-10555-36      Sequence 36, Appl
 30    458.5    66.5   126    5    PCT-US93-08435-14      Sequence 14, Appl
 31    457.5    66.4   126    3    US-08-983-607-48       Sequence 48, Appl
 32    457      66.3   123    4    US-09-240-274-152      Sequence 152, App
 33    455.5    66.1   122    4    US-09-560-198A-4       Sequence 4, Appli
 34    454.5    66.0   135    3    PCT-US93-378A-20       Sequence 20, Appl
 35    454.5    66.0   140    3    US-08-983-607-32       Sequence 32, Appl
 36    454.5    66.0   443    2    US-07-934-373C-4       Sequence 4, Appli
 37    453.5    65.8   120    2    US-08-437-642B-4       Sequence 4, Appli
 38    453.5    65.8   120    4    US-08-146-206C-4       Sequence 4, Appli
 39    453.5    65.8   112    4    US-08-211-202-133      Sequence 133, App
 40    453      65.7   121    1    US-08-887-352B-4       Sequence 4, Appli
 41    453      65.7   121    3    US-09-296-005-4        Sequence 4, Appli
 42    453      65.7   121    3    US-09-109-207C-4       Sequence 4, Appli
 43    453      65.7   121    3    US-08-428-197-1        Sequence 1, Appli
 44    453      65.7   125    3    US-08-428-197-1        Sequence 1, Appli
 45    453      65.7   125    5    PCT-US93-10555-1       Sequence 1, Appli
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ALIGNMENTS

```
RESULT 1
US-09-240-274-28

; Sequence 28, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 28
;   LENGTH: 131
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain E03
US-09-240-274-28

  Query Match          100.0%;  Score 689;  DB 3;  Length 131;
  Best Local Similarity 100.0%;  Pred. No. 6.1e-58;
  Matches 131;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy         1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
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Db         1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60

Qy        61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120

Qy       121 WGQGTTVIVSS 131
             |||||||||||
Db       121 WGQGTTVIVSS 131


RESULT 2
US-09-240-274-27

; Sequence 27, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
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FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 27
  LENGTH: 127
  TYPE: PRT
  ORGANISM: Homo sapiens
  FEATURE:
  OTHER INFORMATION: anti-Rh(D) chain E01is
US-09-240-274-27

Query Match   93.3%;
Best Local Similarity 95.4%;
Matches 125; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

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Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
         |||||      |||||||||||||||||||||||||||||||||||||||||||||
Db   1 EVQLL---ESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQAPGKGLEWVSSISNSNT 56

Qy  61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  57 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDSRYSNFLRWVRSDGMDV 116

Qy 121 WGQGTTVIVSS 131
         |||||||||||
Db 117 WGQGTTVIVSS 127
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RESULT 3
US-08-918-148-78
Sequence 78, Application US/08918148A
Patent No. 6342220
GENERAL INFORMATION:
APPLICANT: Adams, Camellia
APPLICANT: Carter, Paul J.
APPLICANT: W
APPLICANT: Fendly, Brian M.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: P0979
CURRENT APPLICATION NUMBER: US/08/918,148A
CURRENT FILING DATE: 1997-08-25
NUMBER OF SEQ ID NOS: 79
SEQ ID NO 78
  LENGTH: 245
  TYPE: PRT
  ORGANISM: artificial
  FEATURE:
  NAME/KEY: unknown
  LOCATION: 208
  OTHER INFORMATION: unknown amino acid
US-08-918-148-78

Query Match   73.7%; Score 507.5; DB 4; Length 245;
Best Local Similarity 77.9%; Pred. No. 1.6e-40;
Matches 102; Conservative 9; Mismatches 7; Indels 13; Gaps 2;

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Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
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Db   3 QVQL-----VESGGGLVKPGGSLRLSCAASGFTFSSHNMWVRQAPGKGLEWVSSISSSS 58

Qy  61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
         ||||||::||||||||||||||||||||||||||:|||||||||
Db  59 YIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDR--------GSTGMDV 109

Qy 121 WGQGTTVIVSS 131
         ||:|| | |||
Db 121 WGQGTTVIVSS 131
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Db 110 WGRGTLVTVSS 120

RESULT 4
US-10-039-785-53
Sequence 53, Application US/10039785
Patent No. 6538938
GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: US/331,310
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/331,044
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/327,364
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/323,807
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/309,176
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/293,473
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 53
  LENGTH: 249
  TYPE: PRT
  ORGANISM: Artificial sequence
  FEATURE:
  OTHER INFORMATION: T1006F07 scFv
US-10-039-785-53

Query Match   70.8%; Score 488; DB 4; Length 249;
Best Local Similarity 75.8%; Pred. No. 1.1e-38;
Matches 100; Conservative 9; Mismatches 15; Indels 8; Gaps 3;

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Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
         ||||| |||||||||:|||||||||||||||||||| :||||||||||||||:
Db   1 EVQLL---ESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGG 56

Qy  61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVR-SDGMD 119
         ||||||::||||||||||||:||::|||||||||:|||||||||   :|   :| |||
Db  57 STYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARE---PSFQQWGHYSYGMD 113

Qy 120 VWGQGTTVIVSS 131
         |||||| | |||
Db 114 VWGQGTMVTVSS 125
```

RESULT 5
US-08-379-057-32
Sequence 32, Application US/08379057
Patent No. 5876950
GENERAL INFORMATION:
APPLICANT: Siadak, Anthony W.
APPLICANT: Hollenbaugh, Diane L.
APPLICANT: Gilliland, Lisa K.
APPLICANT: Gordon, Marcia L.
APPLICANT: Bajorath, Jurgen
APPLICANT: Aruffo, Alejandro A.
TITLE OF INVENTION: Monoclonal Antibodies Specific For
TITLE OF INVENTION: Different Epitopes of Human gp39 and Methods For Their Use
TITLE OF INVENTION: In Diagnosis and Therapy

NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company
STREET: 3005 First Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,057
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Poor, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0133-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 727-3601
TELEFAX: (206) 727-3670
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-379-057-32

Query Match   69.9%; Score 481.5; DB 2; Length 109;
Best Local Similarity   76.9%; Pred. No. 1.8e-38;
Matches 100; Conservative 4; Mismatches 5; Indels 21; Gaps 3;

Qy   1 EVQLLESGVESGGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
         |||| |||||||||||||||||||||||||||||||||||| ||||||||| :::
Db   1 EVQL----VESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQAPGKGLEWVSSIS-SSS 55

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
         |||||| :||||||||||||||||||||||||||| ||||||| |
Db   56 YIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR------------DY 99

Qy 121 WGQGTTVTVS 130
         |||||| | ||
Db 100 WGQGTLVTVS 109

RESULT 6
US-08-665-202-30
Sequence 30, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: Tumor Antigens
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER.: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER.: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER.: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 023078-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-30

Query Match   69.8%; Score 481; DB 2; Length 123;
Best Local Similarity   76.5%; Pred. No. 2.3e-38;
Matches 101; Conservative 8; Mismatches 13; Indels 10; Gaps 4;

Qy   1 EVQLLESGVESGGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
         |||| |||||||||:|||||||||||||||||||| :|||:||||||||: :::
Db   1 QVQL----VESGGGLVQPGGSLRLSCAASGFTFSSYEMNWVRQAPGKGLEWVSYISSGS 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARD-SRYSNFLRWVRSDGMD 119
         |||||| :||||||||||||||||||||||||||| |||||||| :| :| |:|
Db   57 TIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLGGYS--YGYV---GLD 111

Qy 120 VWGQGTTVTVSS 131
         |||||| | |||
Db 112 YWGQGTLVTVSS 123

RESULT 7
US-09-315-574-30
Sequence 30, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: Tumor Antigens
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250

; FILING DATE: 15-JUN-1995
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/665,202
;   FILING DATE: 13-JUN-1996
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hunter, Tom
;   REGISTRATION NUMBER: 38,498
;   REFERENCE/DOCKET NUMBER: 02307E-061411
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 576-0200
;   TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 30:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 123 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-09-315-574-30

Query Match   69.8%; Score 481; DB 4; Length 123;
Best Local Similarity 76.5%; Pred. No. 2.3e-38;
Matches 101; Conservative 8; Mismatches 13; Indels 10; Gaps 4;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
        |||| |:|||||||||||||||||||||||||||||||||||||| ||||:|:::
Db   1 QVQL----VESGGGLVQPGGSLRLSCAASGFTFSSYEMNWVRQAPGKGLEWVSYISSGS 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARD-SRYSNFLRWVRSDGMD 119
        |||||:|||||||||||||||||||||||||||||||:||||| || : |||
Db   57 TIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLGGYS--YGYV---GLD 111

Qy 120 YWGQGTTVIVSS 131
        |||||||:|||
Db 112 YWGQGTLVTVSS 123

RESULT 8
US-08-918-148-75
Sequence 75, Application US/08918148A
Patent No. 6342220
GENERAL INFORMATION:
  APPLICANT: Adams, Camellia
  APPLICANT: W.
  APPLICANT: Carter, Paul J.
  APPLICANT: Fendly, Brian M.
  APPLICANT: Gurney, Austin L.
  TITLE OF INVENTION: Agonist Antibodies
  FILE REFERENCE: P0979
  CURRENT APPLICATION NUMBER: US/08/918,148A
  CURRENT FILING DATE: 1997-08-25
  NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 75
;   LENGTH: 245
;   TYPE: PRT
;   ORGANISM: artificial
US-08-918-148-75

Query Match   69.6%; Score 479.5; DB 4; Length 245;
Best Local Similarity 72.5%; Pred. No. 7.1e-38;
Matches 95; Conservative 8; Mismatches 15; Indels 13; Gaps 2;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
        |||| :|||||||||||||||||||||||||||||||:||||||||||||||:|:::
Db   3 EVQL----VQSGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSGS 58

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
        |||||:|||||||||||||||||||||||||||||||:|| || :|||
Db   59 TIYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCA-------RWSGEDAFDI 109

Qy 121 WGQGTTVIVSS 131
        |||||| : |||
Db 110 WGQGTMVTVSS 120

RESULT 9
US-08-211-202-134
Sequence 134, Application US/08211202
Patent No. 5565332
GENERAL INFORMATION:
  APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matteus
  APPLICANT: BAIER, Michael
  APPLICANT: JESPERS, Laurent Stephane Anne Therese
  APPLICANT: WINTER, Gregory Paul
  TITLE OF INVENTION: Production of chimeric antibodies - a
  TITLE OF INVENTION: combinatorial approach
  NUMBER OF SEQUENCES: 144
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
  ADDRESSEE: Borun
  STREET: 6300 Sears Tower, 233 South Wacker Drive
  CITY: Chicago
  STATE: Illinois
  COUNTRY: USA
  ZIP: 60606-6402
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/211,202
  FILING DATE: 23-SEP-1992
  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: GB 9120252.3
  FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: GB 9120377.8
  FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: GB 9206318.9
  FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: GB 9206372.6
  FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: PCT/GB92/00883
  FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
  NAME: David W. Clough
  REGISTRATION NUMBER: 36,107
  REFERENCE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 312-474-6300
  TELEFAX: 312-474-0448
  TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 134:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 111 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-211-202-134

Query Match   69.4%; Score 478.5; DB 1; Length 111;
Best Local Similarity 78.2%; Pred. No. 3.5e-38;
Matches 97; Conservative 7; Mismatches 7; Indels 13; Gaps 2;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
        |||| :||||||||||||||||||||||||||||||||||||||||||:|:::
Db   1 EVQL----VQSGGGLVQPGGSLRLSCAASGFTFSSYEMNWVRQAPGKGLEWVSYISSSS 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
        |||||:|||||||||||||||||||||||||||||:|| || :|||
Db   57 TIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARS-------VDSYGMDV 107

RESULT 10
US-08-082-623-3
Sequence 3, Application US/08082623
Patent No. 5750106

GENERAL INFORMATION:
APPLICANT: Ostberg, Lars G.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO
TITLE OF INVENTION: CYTOMEGALOVIRUS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/082,623
FILING DATE: 25-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/010,228
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-055-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..123
OTHER INFORMATION: /note= "The peptide sequence fo the
OTHER INFORMATION: V-h region of SD2 MSL 109."
US-08-082-623-3

Query Match   68.7%; Score 473.5; DB 1; Length 123;
Best Local Similarity   75.4%; Pred. No. 1.2e-37;
Matches   92; Conservative 10; Mismatches 17; Indels 3; Gaps 1;

```
Qy    6  ESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNTYIYYA   65
            ||||||||||||||||||||||||||| |||  ||||||||||||||||::||| |||
Db    2  EQVLESGGGLVKPGGSLRLSCAASGFTFSPYSVFWVRQAPGKGLEWVSSINSDSTYKYYA   61

Qy   66  DAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSD---GMDVWG  122
            |:|||||||||||:||: |||||||||:|||||||||||  |       |  :||||
Db   62  DSVKGRFTISRDNAENSIFLQMNSLRAEDTAVYYCARDRSYYAFSSGSLSDYYYGLDVWG  121

Qy  121  WGQG  124
            ||||
Db  108  WGQG  111
```

RESULT 11
US-08-478-039-102
Sequence 102, Application US/08478039
Patent No. 5681722

GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,039
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: not relevant
STRANDEDNESS: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: #40
US-08-478-039-102

Query Match   68.3%; Score 470.5; DB 1; Length 128;
Best Local Similarity   72.7%; Pred. No. 2.4e-37;
Matches   96; Conservative 9; Mismatches 22; Indels 5; Gaps 2;

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Qy    1  EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT   60
         ||||   |:||||||||:||||||||||||||||||  ||||||||||||||  |::: :
Db    1  EVQL----VESGGGLVQPGGSLRLSCAASGFTFSSYDMNWVRQAPGKGLEWVXYISSASG   56

Qy   61  YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRW-VRSDGMD  119
         ||||||:||||||||||| |||||:|||:|||||:|||||||||     :  | | :  :
Db   57  YIYYADSVKGRFTISRDFAKNSLSLQMSSLRAEDTAVYYCARGQPVLQFLEWLLPTTGSD  116

Qy  120  VWGQGTTVTVSS  131
         |||| |  | ||
Db  117  VWGPGVLVTVSS  128
```

RESULT 12
US-08-476-349A-102
Sequence 102, Application US/0847349A
Patent No. 5750105
GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: #40
US-08-476-349A-102

Query Match   68.3%; Score 470.5; DB 1; Length 128;
Best Local Similarity 72.7%; Pred. No. 2.4e-37;
Matches 96; Conservative 9; Mismatches 22; Indels 5; Gaps 2;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
            |||| ||:||||||||||||||||:||||||||||||| |||||||
Db   1 EVQL----VESGGGLVQPGGSLRLSCAASGFTFSSYDMNWVRQAPGKGLEWVXYISSASG 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRW-VRSDGMD 119
            |||||:|||||||||||| |||| |||:||||| |||||||||:|
Db   57 YIYYADSVKGRFTISRDFAKNSLSLQMSSLRAEDTAVYYCARGQPVLQFLEWLLPTTGSD 116

Qy   120 VWGQGTTVISS 131
            ||| | |||
Db   117 VWGPGVLVTVSS 128

RESULT 13
US-09-025-769B-24
Sequence 24, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-24

Query Match   68.2%; Score 470; DB 4; Length 117;
Best Local Similarity 73.3%; Pred. No. 2.4e-37;
Matches 96; Conservative 5; Mismatches 16; Indels 14; Gaps 2;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
            |||| |||||||||||||||||||||||||||||| |||:||||||||||| ||
Db   1 EVQL----VESGGGLVQPGGSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVSVISYDGG 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWRWVRSDGMDV 120
            |:|||||||||||||||:|||||||||||||||||||||
Db   57 NTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARD----------RGGSGDY 106

Qy   121 WGQGTTVIVSS 131
            ||| |||||
Db   107 WGQGTLVTVSS 117

RESULT 14
US-09-560-198A-2
Sequence 2, Application US/09560198A
Patent No. 6492497
; GENERAL INFORMATION:

```
;  APPLICANT: Thompson, Julia E
;  APPLICANT: Lennard, Simon N
;  APPLICANT: Wilton, Alison J
;  APPLICANT: Braddock, Peta SH
;  APPLICANT: Du Fou, Sarah L
;  APPLICANT: McCafferty, John G
;  APPLICANT: Conroy, Louise A
;  APPLICANT: Tempest, Philip R
;  TITLE OF INVENTION: Specific binding members for TGFbeta1
;  FILE REFERENCE: 28111/35620A
;  CURRENT APPLICATION NUMBER: US/09/560,198A
;  CURRENT FILING DATE: 2000-04-28
;  PRIOR APPLICATION NUMBER: US 60/131,983
;  PRIOR FILING DATE: 1999-04-30
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.1
;
;  SEQ ID NO 2
;    LENGTH: 123
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-560-198A-2

Query Match            68.2%;   Score 470;   DB 4;   Length 123;
Best Local Similarity  70.2%;   Pred. No. 2.5e-37;
Matches   92;  Conservative  14;   Mismatches  17;   Indels   8;   Gaps   2;

Qy     1  EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPCKGLEWVSSISNSNT  60
          :||| :   :|: || ||||||||||||||||||:|||||||||:||:: |||:|||:|||
Db     1  QVQL----VQSGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGS  56

Qy    61  YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV  120
          ||:|||||||||||||||||| ||||||||||||| |:|||||||| ||   :   |::
Db    57  IKIYADSVKGRFTISRDNSKNTLILQMNSLRAEDTAVYYCARTGEYSGY-----DTSGVEL  112

Qy   121  WGQGTTVIVSS  131
          |||||||| |||
Db   113  WGQGTTVTVSS  123
```

```
RESULT 15
US-08-478-039-73
;  Sequence 73, Application US/08478039
;  Patent No. 5681722
;  GENERAL INFORMATION:
;    APPLICANT: Newman, Roland A.
;    APPLICANT: Hanna, Nabil
;    APPLICANT: Raab, Ronald W.
;  TITLE OF INVENTION:  Recombinant Antibodies for Human Therapy
;  NUMBER OF SEQUENCES:  114
;  CORRESPONDENCE ADDRESS:
;    ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;    STREET:  699 Prince St.
;    CITY:  Alexandria
;    STATE:  VA
;    COUNTRY:  USA
;    ZIP:  22313-1404
;  COMPUTER READABLE FORM:
;    MEDIUM TYPE:  Floppy disk
;    COMPUTER:  IBM PC compatible
;    OPERATING SYSTEM:  PC-DOS/MS-DOS
;    SOFTWARE:  PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;    APPLICATION NUMBER:  US/08/478,039
;    FILING DATE:  07-JUN-1995
;    CLASSIFICATION:  435
;  PRIOR APPLICATION DATA:
;    APPLICATION NUMBER:  US 08/379,072
;    FILING DATE:  25-JAN-1995
;  PRIOR APPLICATION DATA:
;    APPLICATION NUMBER:  US 07/912,292
;    FILING DATE:  10-JUL-1992
;  PRIOR APPLICATION DATA:
;    APPLICATION NUMBER:  US 07/856,281
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;    FILING DATE:  23-MAR-1992
;  PRIOR APPLICATION DATA:
;    APPLICATION NUMBER:  US 07/735,064
;    FILING DATE:  25-JUL-1991
;  ATTORNEY/AGENT INFORMATION:
;    NAME:  Teskin Esq., Robin L.
;    REGISTRATION NUMBER:  35,030
;    REFERENCE/DOCKET NUMBER:  012712-160
;  TELECOMMUNICATION INFORMATION:
;    TELEPHONE:  703-836-6620
;    TELEFAX:  703-836-2021
;  INFORMATION FOR SEQ ID NO:  73:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  128 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  peptide
;    ORIGINAL SOURCE:
;    ORGANISM:  Monkey
;    POSITION IN GENOME:
;    CHROMOSOME/SEGMENT:  VH3 clone 3-40
US-08-478-039-73

Query Match            68.1%;   Score 469.5;   DB 1;   Length 128;
Best Local Similarity  72.0%;   Pred. No. 2.9e-37;
Matches   95;  Conservative  10;   Mismatches  22;   Indels   5;   Gaps   2;

Qy     1  EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT  60
          |||| :    :|||| :|||||||||||||||||:||||||||| :|:: |||:|||:|||
Db     1  EVQL----VESGGGLVQPGGSLRLSCAASGFTFSSYDMNWVRQAPGKGLEWVSSISSASG  56

Qy    61  YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRW-VRSDGMD  119
          ||:|||:||||||||||||:||| :|||||||||:|||||||| ::|||||||   |  |
Db    57  YIYYADSVKGRFTISRDFSKNTLSLQMNSLRAEDTAVYYCARGQPVLQFLEWLLPTTGSD  116

Qy   120  VWGQGTTVIVSS  131
          |||| | |||
Db   117  VWGPGVLVTVSS  128
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Search completed: September 24, 2003, 06:30:34
Job time : 36 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 24, 2003, 06:29:06 ; Search time 467 Seconds
                                                (without alignments)
                                                42.444 Million cell updates/sec

Title: US-09-848-798A-28
Perfect score: 689
Sequence: 1 EVQLLESGVESGGGGLVKPGG.........WVRSDGMDVWGQGTTVIVSS 131

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 566894 seqs, 15130793 residues

Total number of hits satisfying chosen parameters: 566894

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_AA:*
                 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
                 2: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                 3: /cgn2_6/ptodata/2/pubpaa/US06_PCT_NEW_PUB.pep:*
                 4: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
                 5: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
                 6: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
                 8: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
                 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
                 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
                 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
                 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
                 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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                 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	% Query Match	Length	DB	ID	Description
1	689	100.0	131	11	US-09-848-798-28	Sequence 28, Appl
2	643	93.3	127	11	US-09-880-748-27	Sequence 27, Appl
3	511.5	74.2	256	11	US-09-880-748-1318	Sequence 1318, Ap
4	509	73.9	248	11	US-09-880-748-913	Sequence 913, App
5	506.5	73.5	247	11	US-09-880-748-1764	Sequence 1764, Ap
6	504.5	73.2	116	15	US-10-091-300-24	Sequence 24, Appl
7	499.5	72.5	116	15	US-10-091-300-31	Sequence 31, Appl
8	499.5	72.5	249	11	US-09-880-748-1856	Sequence 1856, Ap
9	498	72.3	241	11	US-09-880-748-1937	Sequence 1937, Ap
10	497.5	72.2	247	11	US-09-880-748-1703	Sequence 1703, Ap
11	495.5	71.9	249	11	US-09-880-748-974	Sequence 974, App
12	494.5	71.8	248	11	US-09-880-748-1974	Sequence 1974, Ap
13	493.5	71.6	262	11	US-09-880-748-2081	Sequence 2081, Ap
14	492.5	71.5	252	11	US-09-880-748-1634	Sequence 1634, Ap
15	491.5	71.3	128	10	US-09-840-459-77	Sequence 77, Appl
16	491.5	71.3	128	10	US-09-840-459-79	Sequence 79, Appl
17	491	71.3	250	11	US-09-880-748-1179	Sequence 1179, Ap
18	491	71.3	255	11	US-09-880-748-1608	Sequence 1608, Ap
19	489.5	71.0	248	11	US-09-880-748-1965	Sequence 1965, Ap
20	489	71.0	244	11	US-09-880-748-1991	Sequence 1991, Ap
21	488	70.8	249	13	US-10-039-785-53	Sequence 53, Appl
22	487.5	70.8	256	11	US-09-880-748-1209	Sequence 1209, Ap
23	487.5	70.8	258	11	US-09-880-748-1841	Sequence 1841, Ap
24	485.5	70.5	250	11	US-09-880-748-1613	Sequence 1613, Ap
25	485	70.4	127	10	US-09-840-459-87	Sequence 87, Appl
26	484	70.2	255	11	US-09-880-748-1819	Sequence 1819, Ap
27	483	70.1	121	10	US-09-840-459-92	Sequence 92, Appl
28	483	70.1	125	10	US-09-840-459-76	Sequence 76, Appl
29	482.5	70.0	252	11	US-09-880-748-1362	Sequence 1362, Ap
30	482.5	70.0	253	12	US-09-880-748-2104	Sequence 76, Appl
31	480.5	69.7	237	11	US-09-880-748-2104	Sequence 2104, Ap
32	480.5	69.7	240	11	US-09-880-748-2105	Sequence 2105, Ap
33	480.5	69.7	240	11	US-09-880-748-2113	Sequence 2113, Ap
34	480.5	69.6	126	10	US-10-041-860-13	Sequence 13, Appl
35	479.5	69.6	126	10	US-09-880-748-208	Sequence 208, Appl
36	478.5	69.4	247	11	US-09-880-748-1294	Sequence 1294, Ap
37	478.5	69.4	251	11	US-09-880-748-908	Sequence 908, Appl
38	478	69.3	120	11	US-09-995-529-8	Sequence 8, Appli
39	477.5	69.3	126	12	US-10-041-860-270	Sequence 270, App
40	477.5	69.3	237	11	US-09-880-748-2020	Sequence 2020, Ap
41	477.5	69.3	444	15	US-10-150-475A-6	Sequence 6, Appli
42	477	69.2	138	12	US-10-325-694-144	Sequence 144, App
43	477	69.2	138	12	US-10-325-694-150	Sequence 150, App
44	476	69.1	243	11	US-09-880-748-2102	Sequence 2102, Ap
45	475.5	69.0	254	11	US-09-880-748-1701	Sequence 1701, Ap

ALIGNMENTS

RESULT 1
US-09-848-798-28

Sequence 28, Application US/09848798
Publication No. US20030040605A1

GENERAL INFORMATION:
  APPLICANT: Siegel, Donald L.
  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
  FILE REFERENCE: 09596-42U2
  CURRENT APPLICATION NUMBER: US/09/848,798
  CURRENT FILING DATE: 2001-05-04
  PRIOR APPLICATION NUMBER: US/09/848,798
  PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 09/240,274
  PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-01-29
  PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 60/028,550
  PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1996-10-11
  NUMBER OF SEQ ID NOS: 224
  SOFTWARE: Patentin Ver. 2.0
  SEQ ID NO 28
    LENGTH: 131
    TYPE: PRT
    ORGANISM: Homo sapiens
    FEATURE:
    OTHER INFORMATION: anti-Rh(D) chain E03
US-09-848-798-28

Query Match   100.0%; Score 689; DB 11; Length 131;
Best Local Similarity   100.0%; Pred. No. 8.1e-56;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 EVQLLESGVESGGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPCKGLEWVSISNSNT 60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 EVQLLESGVESGGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPCKGLEWVSISNSNT 60

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120

Qy   121 WGQGTTVIVSS 131
             |||||||||||
Db   121 WGQGTTVIVSS 131

Db   121 WGQGTTVIVSS 131
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RESULT 2
US-09-848-798-27
Sequence 27, Application US/09848798
Publication No. US20030040605A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09,848,798
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 27
LENGTH: 127
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain E011s
US-09-848-798-27

Query Match   93.3%;   Score 643;   DB 11;   Length 127;
Best Local Similarity   95.4%;
Matches 125;   Conservative   0;   Mismatches   2;   Indels   4;   Gaps   1;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
         ||||| |:|||||||||||||||||||||||||||||||||||||||||||||||:::
Db   1 EVQLL----ESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQAPGKGLEWVSSISSSS 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   57 YIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDSRYSNFLRWVRSDGMDV 116

Qy 121 WGQGTTVIVSS 131
         |||||||||||
Db 117 WGQGTTVIVSS 127

RESULT 3
US-09-880-748-1318
Sequence 1318, Application US20030059937A1
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09,880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1318
LENGTH: 256
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1318

Query Match   74.2%;   Score 511.5;   DB 11;   Length 256;
Best Local Similarity   78.2%;   Pred. No. 2.8e-39;
Matches 104;   Conservative 11;   Mismatches 11;   Indels   7;   Gaps   3;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
         ||| |:||||||||||||||||||||||||||||||||||||:||||||||:||
Db   1 EVQL----VQSCGGLVKPGGSLRLSCAASGFTFSSYSMWVRQAPGKGLEWVSSISSSS 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 117
         ||||:|:||||||||||||||||||||||||||||:||||||| : | ||:
Db   57 YIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLGSFYDILTALRLENYG 116

Qy 118 MDVWGQGTTVIVS 130
         ||||:||| |||
Db 117 MDVWGKGTLVTVS 129

RESULT 4
US-09-880-748-913
Sequence 913, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09,880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 913
LENGTH: 248
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-913

Query Match   73.9%;   Score 509;   DB 11;   Length 248;
Best Local Similarity   78.6%;   Pred. No. 4.6e-39;
Matches 103;   Conservative   8;   Mismatches 14;   Indels   6;   Gaps   2;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
         |||| |:|||:|||||||||||||||||||||||||:|||||||||||||||||:|
Db   1 EVQL----VESGGGLVQPGGSLRLSCAAFGFTFSSYSMWVRQAPGKGLEWVSSISNRGS 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
         ||||:|:||||||||||||||||||||||||||||:||||:|:::| | ||
Db   57 YIYYADSVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYCAREGR--DILTGVYYGLDV 114

Qy 121 WGQGTTVIVSS 131
         |||||| ||
Db 115 WGQGTLVTVSS 125

RESULT 5
US-09-880-748-1764
Sequence 1764, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09,880,748
CURRENT FILING DATE: 2001-06-15

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; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
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; SEQ ID NO 1764
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1764

Query Match             73.5%;  Score 506.5;  DB 11;  Length 247;
Best Local Similarity   78.6%;  Pred. No. 7.8e-39;
Matches  103;  Conservative  10;  Mismatches  11;  Indels  7;  Gaps  3;

Qy     1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
          :|||||||||||||||||||||||||||||||||||||||||||||||||||:||:::
Db     1 QVQL----VQSGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSS 56

Qy    61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
         |||||:|||||||||||||||||||||||||:||||||| ||  :: ||||||
Db    57 YIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARD-EYDILTGLLQ--GMDV 113

Qy   121 WGQGTTVIVSS 131
         |:|||| | |||
Db   114 WGKGTLVIVSS 124
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RESULT 6
US-10-091-300-24
Sequence 24, Application US/10091300
Publication No US20030108545A1
GENERAL INFORMATION:
APPLICANT: Rockwell, Patricia
APPLICANT: Goldstein, Neil I.
TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth With a Vascular
TITLE OF INVENTION: Endothelial Growth Factor Receptor Antagonist
FILE REFERENCE: 11245/46211
CURRENT APPLICATION NUMBER: US/10/091,300
CURRENT FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 85
SOFTWARE: WordPerfect 8.0 for Windows
;
; SEQ ID NO 24
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Human
US-10-091-300-24

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Query Match             73.2%;  Score 504.5;  DB 15;  Length 116;
Best Local Similarity   77.1%;  Pred. No. 5.3e-39;
Matches  101;  Conservative  8;  Mismatches  7;  Indels  15;  Gaps  2;

Qy     1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
          :|||||||||||||||||||||||||||||||||||||||||||||||||||:||:::
Db     1 EVQL----VQSGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSS 56

Qy    61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
         |||||:|||||||||||||||||||||||||:||||||||
Db    57 YIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR------------VTDAFDI 105

Qy   121 WGQGTTVIVSS 131
         |:||| | |||
Db   106 WGQGTMVIVSS 116
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RESULT 7

US-10-091-300-31
Sequence 31, Application US/10091300
Publication No. US20030108545A1
GENERAL INFORMATION:
APPLICANT: Rockwell, Patricia
APPLICANT: Goldstein, Neil I.
TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth With a Vascular
TITLE OF INVENTION: Endothelial Growth Factor Receptor Antagonist
FILE REFERENCE: 11245/46211
CURRENT APPLICATION NUMBER: US/10/091,300
CURRENT FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 85
SOFTWARE: WordPerfect 8.0 for Windows
;
; SEQ ID NO 31
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Human
US-10-091-300-31

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Query Match             72.5%;  Score 499.5;  DB 15;  Length 116;
Best Local Similarity   76.3%;  Pred. No. 1.5e-38;
Matches  100;  Conservative  9;  Mismatches  7;  Indels  15;  Gaps  2;

Qy     1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
          :|||||||||||||||||||||||||||||||||||||||||||||||||||:||:::
Db     1 EVQL----VQSGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSS 56

Qy    61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
         |||||:|||||||||||||||||||||||||:||||||||
Db    57 YIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR------------VTDAFDI 105

Qy   121 WGQGTTVIVSS 131
         |:||| | |||
Db   106 WGQGTMVTVSS 116
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RESULT 8
US-09-880-748-1856
Sequence 1856, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 1856
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1856

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Query Match             72.5%;  Score 499.5;  DB 11;  Length 249;
Best Local Similarity   78.6%;  Pred. No. 3.4e-38;
Matches  103;  Conservative  7;  Mismatches  14;  Indels  7;  Gaps  3;

Qy     1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
          :|||||||||||||||||||||||||||||||||||||||||||||||||||:||:::
Db     1 EVQL----VESGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSS 56

Qy    61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
```

RESULT 9
US-09-880-748-1937
; Sequence 1937, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1937
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1937

Query Match   72.3%; Score 498; DB 11; Length 241;
Best Local Similarity 77.7%; Pred. No. 4.5e-38;
Matches 101; Conservative 7; Mismatches 8; Indels 14; Gaps 2;

Qy   2 VQLLESGVESGGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNTY 61
            |:| | |:||||||||||||||||||||||:||| ||||||||||||||||||:||:::|
Db   2 VQL-----VQSGGGLVKSGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISISSSY 57

Qy   62 IYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDVW 121
            |||||| ||||||||||||||||||||||||:|| |||||||||| |:| | |||| |||
Db   58 IYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGHFY-------GMDVW 107

Qy   122 GQGTTVIVSS 131
            ||:|| |||
Db   108 GRGTMVTVSS 117

RESULT 10
US-09-880-748-1703
; Sequence 1703, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1703
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1703

Query Match   72.2%; Score 497.5; DB 11; Length 247;
Best Local Similarity 78.6%; Pred. No. 5.2e-38;
Matches 103; Conservative 8; Mismatches 13; Indels 13; Gaps 3;

Qy   1 EVQLLESGVESGGGGLVKRPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
            :||| | |:|||||||| |||||||||||||||||||||:||| |||||||||||:|:::
Db   1 QVQL-----VESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISISSSS 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
            |||||| ||||||||||||||||||||||||:|| |||||||| | |:| ||| | |
Db   57 YIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCA-TLGYDILTGYRDY 113

Qy   121 WGQGTTVIVSS 131
            | :||| |||
Db   114 WGKGTLVTVSS 124

RESULT 11
US-09-880-748-974
; Sequence 974, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 974
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-974

Query Match   71.9%; Score 495.5; DB 11; Length 249;
Best Local Similarity 76.5%; Pred. No. 8e-38;
Matches 101; Conservative 11; Mismatches 13; Indels 7; Gaps 3;

Qy   1 EVQLLESGVESGGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
            :||| | | |:||||||||||||||||||||||||||||||:||| |||||||||||:::
Db   1 EVQL-----VQSGGGLVKPGGSLRLSCAASGFTFSNTWMTWVRQAPGKGLEWVSSISISSSS 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSD-GMD 119
            |||||| ||||||||||||||||||||||||:|| |||||||: | |:| ||| | |:|
Db   57 YIYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARE--YYDILTGYRDPYGMD 114

Qy   120 VWGQGTTVIVSS 131
            |||:||| ||||
Db   115 VWGQGTMVTVSS 126

RESULT 12
US-09-880-748-1974
; Sequence 1974, Application US/09880748

; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1974
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1974

Query Match   71.8%;   Score 494.5; DB 11; Length 248;
Best Local Similarity   76.3%;   Pred. No. 9.8e-38;
Matches 100;   Conservative 8;   Mismatches 14;   Indels   9;   Gaps   2;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
          |||| |:||||||||||||||||||||||||||||||||||||||||||||||
Db   1 EVQL----VQSGGGLVQPGGSLRLSCAASGFTFSSYEMNWVRQAPGKGLEWVSYISSSGS 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
          ||||||:|||||||||||||||||||||||||||||||||||| | : ||||
Db   57 TIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARSGRQAYYY-----GMDV 111

Qy   121 WGQGTVIVSS 131
          ||:||| |||
Db   112 WGQGTLVSS 122

RESULT 13
US-09-880-748-2081
Sequence 2081, Application US20030059937A1
Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2081
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2081

Query Match   71.6%;   Score 493.5; DB 11; Length 262;
Best Local Similarity   69.9%;   Pred. No. 1.3e-37;
Matches 100;   Conservative 13;   Mismatches   7;   Indels 23;   Gaps   3;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
          |||| |:||||||||||||||||||||||||||||||||||||||||||||||
Db   1 EVQL----VQSGGGLVQPGGSLRLSCAASGFTFSSYEMNWVRQAPGKGLEWVSYISRSSR 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
          ||||||:|||||||||||||||||||||||||||||||||| |:| ||||
Db   57 TIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDSRYSNFLRWVR----- 111

Qy   121 WGQGTVIVSS 131
          ||:||| |||
Db   112 WGQGTLVTVSS 122

RESULT 14
US-09-880-748-1634
Sequence 1634, Application US/09880748
Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1634
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1634

Query Match   71.5%;   Score 492.5; DB 11; Length 252;
Best Local Similarity   73.0%;   Pred. No. 1.5e-37;
Matches 100;   Conservative 11;   Mismatches   9;   Indels 17;   Gaps   3;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
          |||| |:|||||||:|||||||||||||||||||||||||||||||||||||||
Db   1 QVQL----VQSGGGVVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYISSNSNT 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARD-------SRYSNFLRWVR 114
          ||||||:|||||||||||||||||||||||||||:||||||| : |||:
Db   57 SIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDRDYDILTDYSNY----- 111

Qy   115 SDGMDVWGQGTTVIVSS 131
          :|||||||||||| |||
Db   112 --GMDVWGQGTMVTVSS 126

RESULT 15
US-09-840-459-77
Sequence 77, Application US/09840459
Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855,1052-012

```
;  CURRENT APPLICATION NUMBER: US/09/840,459
;  CURRENT FILING DATE: 2001-02-02
;  PRIOR APPLICATION NUMBER: PCT/US01/03537
;  PRIOR FILING DATE: 2001-02-02
;  PRIOR APPLICATION NUMBER: 09/497,625
;  PRIOR FILING DATE: 2000-02-03
;  PRIOR APPLICATION NUMBER: 09/359,193
;  PRIOR FILING DATE: 1999-07-22
;  PRIOR APPLICATION NUMBER: 09/121,781
;  PRIOR FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 107
;  SEQ ID NO 77
;  LENGTH: 128
;  TYPE: PRT
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: VARIANT
;  LOCATION: (1)...(128)
;  OTHER INFORMATION: Xaa = Any Amino Acid
US-09-840-459-77

Query Match          71.3%;  Score 491.5;  DB 10;  Length 128;
Best Local Similarity   75.4%;  Pred. No. 9.1e-38;
Matches 101;  Conservative  8;  Mismatches 16;  Indels   9;  Gaps  3;

Qy         1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
             ||||| ||:|||||||||||||||||||||||:|||||||||||:|||||||:||
Db         1 EVQLL----ESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGG 56

Qy        61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRS---DG 117
             |:||:|:|||||||||||||:|||||||||||||||||||||||| :|  :|   |
Db        57 STYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDRRNYDF--WSGXYYYYG 114

Qy       118 MDVWGQGTTVIVSS 131
             ||||||||||| |||
Db       115 MDVWGQGTTVTVSS 128
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Search completed: September 24, 2003, 06:46:03
Job time : 467 secs

OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: September 24, 2003, 06:26:56 ; Search time 341 Seconds
                       (without alignments)
                       349.558 Million cell updates/sec

Title: US-09-848-798A-28
Perfect score: 689
Sequence: 1 EVQLLESGVESGGGLVKPGG.........WVRSDGMDVWGQGTTVIVSS 131

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 90918778 residues

Total number of hits satisfying chosen parameters: 5728757

Maximum DB seq length: 2000000000
Minimum DB seq length: 0

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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2: /cgn2_6/ptodata/2/paa/US06_COMB.pep:*
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22: /cgn2_6/ptodata/2/paa/US097B_COMB.pep:*
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24: /cgn2_6/ptodata/2/paa/US099A_COMB.pep:*
25: /cgn2_6/ptodata/2/paa/US099B_COMB.pep:*
26: /cgn2_6/ptodata/2/paa/US100_COMB.pep:*
27: /cgn2_6/ptodata/2/paa/US101_COMB.pep:*
28: /cgn2_6/ptodata/2/paa/US102_COMB.pep:*
29: /cgn2_6/ptodata/2/paa/US103_COMB.pep:*
30: /cgn2_6/ptodata/2/paa/US104_COMB.pep:*
31: /cgn2_6/ptodata/2/paa/US106_COMB.pep:*
32: /cgn2_6/ptodata/2/paa/US60_COMB.pep:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length %	Match Length	DB ID	Description
1	689	100.0	131	22	US-09-791-537-71784	Sequence 71784, A

2	689	100.0	131	23	US-09-848-798-28	Sequence 28, Appl
3	689	100.0	131	23	US-09-848-798A-28	Sequence 28, Appl
4	643	93.3	127	22	US-09-791-537-71782	Sequence 71782, A
5	643	93.3	127	23	US-09-848-798-27	Sequence 27, Appl
6	643	93.3	127	23	US-09-848-798A-27	Sequence 27, Appl
7	525	76.2	145	22	US-09-791-537-88960	Sequence 88960, A
8	523	75.9	134	32	US-09-791-537-96307	Sequence 96307, A
9	513.5	74.5	148	22	US-09-791-537-39928	Sequence 39928, A
10	513.5	74.5	128	22	US-09-791-537-90526	Sequence 90526, A
11	511.5	74.2	256	1	PCT-US01-19110-1318	Sequence 1318, Ap
12	511.5	74.2	256	1	PCT-US01-19110-913	Sequence 913, App
13	511.5	74.2	256	23	US-09-880-748-1318	Sequence 1318, Ap
14	511.5	74.2	256	28	US-10-293-418-1318	Sequence 1318, Ap
15	509	73.9	248	1	PCT-US01-19110-913	Sequence 913, App
16	509	73.9	248	1	PCT-US02-36496-913	Sequence 913, App
17	509	73.9	248	1	PCT-US02-36496-913	Sequence 913, App
18	509	73.9	248	28	US-09-880-748-913	Sequence 913, App
19	508.5	73.8	124	29	US-10-308-817-190	Sequence 190, App
20	508.5	73.8	124	23	US-09-880-748-190	Sequence 190, App
21	508.5	73.8	125	22	US-09-791-537-31327	Sequence 31327, A
22	506.5	73.5	247	1	PCT-US01-19110-1764	Sequence 1764, Ap
23	506.5	73.5	247	1	PCT-US02-36496-1764	Sequence 1764, Ap
24	506.5	73.5	247	23	US-09-880-748-1764	Sequence 1764, Ap
25	506.5	73.5	247	28	US-10-293-418-1764	Sequence 1764, Ap
26	506	73.4	240	1	PCT-US03-02612-9	Sequence 9, App11
27	506	73.4	240	26	PCT-US03-02612-9	Sequence 9, App11
28	506	73.4	257	1	PCT-US03-02612-7	Sequence 7, App11
29	506	73.4	257	26	PCT-US03-02612-7	Sequence 7, App11
30	506	73.4	272	32	US-09-791-537-845	Sequence 845, App
31	506	73.4	272	32	US-60-474-850-433	Sequence 433, App
32	505.5	73.4	124	22	US-09-791-537-90523	Sequence 90523, A
33	505.5	73.4	116	1	PCT-US02-06762-24	Sequence 24, Appl
34	504.5	73.2	116	1	PCT-US02-20332-76	Sequence 76, Appl
35	504.5	73.2	116	1	PCT-US02-41372-76	Sequence 76, Appl
36	504.5	73.2	116	1	PCT-US03-06459-24	Sequence 24, Appl
37	504.5	73.2	26	1	US-10-091-300-24	Sequence 24, Appl
38	504.5	73.2	116	32	US-60-361-783-24	Sequence 24, Appl
39	504.5	73.2	126	22	US-09-791-537-116066	Sequence 116066,
40	503.5	73.1	121	22	US-09-791-537-95958	Sequence 95958, A
41	503	73.1	119	22	US-09-791-537-59259	Sequence 59259, A
42	503	73.0	123	22	US-09-791-537-78258	Sequence 78258, A
43	502	72.9	129	22	US-09-791-537-79333	Sequence 79333, A
44	499.5	72.5	116	1	PCT-US02-06762-31	Sequence 31, Appl
45	499.5	72.5	116	1	PCT-US02-20332-83	Sequence 83, Appl

ALIGNMENTS

RESULT 1
US-09-791-537-71784
; Sequence 71784, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 71784
; LENGTH: 131
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-791-537-71784

Query Match   100.0%; Score 689; DB 22; Length 131;
Best Local Similarity   100.0%; Pred. No. 1.9e-62;
Matches 131; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 2
US-09-848-798-28
Sequence 28, Application US/0984879B

GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 28
LENGTH: 131
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain E03

Query Match   100.0%;   Score 689;   DB 23;   Length 131;
Best Local Similarity   100.0%;   Pred. No. 1.9e-62;
Matches 131;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

```
Qy    1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120

Qy  121 WGQGTTVIVSS 131
         |||||||||||
Db  121 WGQGTTVIVSS 131
```

RESULT 3
US-09-848-798A-28
Sequence 28, Application US/09848798A

GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848,798A
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: 1999-05-02
PRIOR APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 131
TYPE: PRT

ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain E03
US-09-848-798A-28

Query Match   100.0%;   Score 689;   DB 23;   Length 131;
Best Local Similarity   100.0%;   Pred. No. 1.9e-62;
Matches 131;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

```
Qy    1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120

Qy  121 WGQGTTVIVSS 131
         |||||||||||
Db  121 WGQGTTVIVSS 131
```

RESULT 4
US-09-791-537-71782
Sequence 71782, Application US/0979153?

GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME...
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 71782
LENGTH: 127
TYPE: PRT
ORGANISM: synthetic construct
US-09-791-537-71782

Query Match   93.3%;   Score 643;   DB 22;   Length 127;
Best Local Similarity   95.4%;   Pred. No. 1e-57;
Matches 125;   Conservative 0;   Mismatches 2;   Indels 4;   Gaps 1;

```
Qy    1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
         |||||    ||||||||||||||||||||||||||||||||||| |||||||||||||||
Db    1 EVQLL----ESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQAPGKGLEWVSSISNSNT 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
         ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   57 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDSRYSNFLRWVRSDGMDV 116

Qy  121 WGQGTTVIVSS 131
         |||||||||||
Db  117 WGQGTTVIVSS 127
```

RESULT 5
US-09-848-798-27
Sequence 27, Application US/09848798

GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11

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;    NUMBER OF SEQ ID NOS: 224
;    SOFTWARE: Patentin Ver. 2.0
;
;    SEQ ID NO 27
;    LENGTH: 127
;    TYPE: PRT
;    ORGANISM: Homo sapiens
;    FEATURE:
;    OTHER INFORMATION: anti-Rh(D) chain E01is
US-09-848-798-27

Query Match      93.3%;   Score 643; DB 23; Length 127;
Best Local Similarity   95.4%;   Pred. No. 1e-57;
Matches 125; Conservative   0; Mismatches   2; Indels   4; Gaps   1;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
        ||||      ||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   1 EVQLL---ESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQAPGKGLEWVSSISNSNT 56

Qy  61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
        |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db  57 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDSRYSNFLRWVRSDGMDV 116

Qy 121 WGQGTTVIVSS 131
        |||||||||||
Db 117 WGQGTTVIVSS 127

RESULT 6
US-09-848-798A-27
Sequence 27, Application US/0984798A
GENERAL INFORMATION:
;    APPLICANT: Siegel, Donald L.
;    TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;    TITLE OF INVENTION:  SORTING METHOD FOR PRODUCTION THEREOF
;    FILE REFERENCE: 09596-4202
;    CURRENT APPLICATION NUMBER: US/09/848,798A
;    CURRENT FILING DATE: 2001-05-04
;    PRIOR APPLICATION NUMBER: 09/240,274
;    PRIOR FILING DATE: 1999-05-02
;    PRIOR APPLICATION NUMBER: 60/028,550
;    PRIOR FILING DATE: 1996-10-11
;    NUMBER OF SEQ ID NOS: 224
;    SOFTWARE: Patentin Ver. 2.0
;
;    SEQ ID NO 27
;    LENGTH: 127
;    TYPE: PRT
;    ORGANISM: Homo sapiens
;    FEATURE:
;    OTHER INFORMATION: anti-Rh(D) chain E01is
US-09-848-798A-27
```

```
;    APPLICANT: Debe, Derek
;    APPLICANT: Danzer, Joseph
;    TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
;    TITLE OF INVENTION: METHODS OF USE THEREOF
;    FILE REFERENCE: 261/210
;    CURRENT APPLICATION NUMBER: US/09/791,537
;    CURRENT FILING DATE: 2001-02-22
;    NUMBER OF SEQ ID NOS: 153055
;    SOFTWARE: Patentin version 3.0
;
;    SEQ ID NO 88960
;    LENGTH: 145
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-791-537-88960

Query Match      76.2%;   Score 525; DB 22; Length 145;
Best Local Similarity   80.9%;   Pred. No. 1.7e-45;
Matches 106; Conservative   7; Mismatches  12; Indels   6; Gaps   2;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
        ||||      ||||||||||||||||||||||||||||| ||||| |||||||| : |
Db  20 EVQL----VESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSS 75

Qy  61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
        ||||| :|||||||||||||||||||||||||| ||||||||| ||::  :  :
Db  76 YIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDVEEATVTYYY--GMDV 133

Qy 121 WGQGTTVIVSS 131
        |||||||:|||
Db 134 WGQGTTVTVSS 144
```

```
RESULT 8
US-09-791-537-96307
Sequence 96307, Application US/09791537
GENERAL INFORMATION:
;    APPLICANT: Bionomix, Inc.
;    APPLICANT: Debe, Derek
;    APPLICANT: Danzer, Joseph
;    TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
;    TITLE OF INVENTION: METHODS OF USE THEREOF
;    FILE REFERENCE: 261/210
;    CURRENT APPLICATION NUMBER: US/09/791,537
;    CURRENT FILING DATE: 2001-02-22
;    NUMBER OF SEQ ID NOS: 153055
;    SOFTWARE: Patentin version 3.0
;
;    SEQ ID NO 96307
;    LENGTH: 134
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-791-537-96307

Query Match      75.9%;   Score 523; DB 22; Length 134;
Best Local Similarity   79.7%;   Pred. No. 2.5e-45;
Matches 106; Conservative   7; Mismatches  14; Indels   6; Gaps   2;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
        ||||      ||||||||||||||||||||||||||| ||||| |||||||| : |
Db   1 EVQL----VESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSS 56

Qy  61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSR--YSNFLRWVRSDGM 118
        ||||| :||||||||||||||||||||||||| |||||||||| |  :
Db  57 YIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGGLLWFGELLSYYYYGM 116

Qy 119 DVWGQGTTVIVSS 131
        ||||||||:||||
Db 117 DVWGQGTTVTVSS 129

RESULT 9
US-09-791-537-39928
Sequence 39928, Application US/09791537
GENERAL INFORMATION:
```

```
RESULT 7
US-09-791-537-88960
Sequence 88960, Application US/09791537
GENERAL INFORMATION:
;    APPLICANT: Bionomix, Inc.

Query Match      93.8%;   Score 643; DB 23; Length 127;
Best Local Similarity   95.4%;   Conservative   0; Mismatches   2; Indels   4; Gaps   1;
Matches 125;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
        ||||      |||||||||||||||||||||||||||||||| |||||||||||||||||
Db   1 EVQLL---ESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQAPGKGLEWVSSISNSNT 56

Qy  61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
        |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db  57 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDSRYSNFLRWVRSDGMDV 116

Qy 121 WGQGTTVIVSS 131
        |||||||||||
Db 117 WGQGTTVIVSS 127
```

```
;   APPLICANT: Bionomix, Inc.
;   APPLICANT: Debe, Derek
;   APPLICANT: Danzer, Joseph
;   TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;   FILE REFERENCE: 261/210
;   CURRENT APPLICATION NUMBER: US/09/791,537
;   CURRENT FILING DATE: 2001-02-22
;   SOFTWARE: Patentin version 3.0
;   NUMBER OF SEQ ID NOS: 153055
;   SEQ ID NO 39928
;     LENGTH: 148
;     TYPE: PRT
;     ORGANISM: Homo sapiens
US-09-791-537-39928

Query Match             74.5%;   Score 513.5;   DB 22;   Length 148;
Best Local Similarity   80.2%;   Pred. No. 2.6e-44;
Matches  105;  Conservative   7;  Mismatches  10;  Indels   9;  Gaps   3;

Qy    1 EVQLLESGVESGGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
          ||||| ::|:||||||||||||||||||||||||||:|||||||||||:::||::
Db   20 EVQL----VESGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYSISSSS 75

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
          |||| | |||||||||||||||||||||||||||:|||:| | |
Db   76 YIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLRG----QWL-VQGEDY 130

Qy  121 WGQGTTVIVSS 131
          ||||| | |||
Db  131 WGQGTLVTVSS 141
```

```
RESULT 10
US-09-791-537-90526
; Sequence 90526, Application US/09791537
; GENERAL INFORMATION:
;   APPLICANT: Bionomix, Inc.
;   APPLICANT: Debe, Derek
;   APPLICANT: Danzer, Joseph
;   TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;   TITLE OF INVENTION: METHODS OF USE THEREOF
;   FILE REFERENCE: 261/210
;   CURRENT APPLICATION NUMBER: US/09/791,537
;   CURRENT FILING DATE: 2001-02-22
;   NUMBER OF SEQ ID NOS: 153055
;   SOFTWARE: Patentin version 3.0
;   SEQ ID NO 90526
;     LENGTH: 128
;     TYPE: PRT
;     ORGANISM: Homo sapiens
US-09-791-537-90526

Query Match             74.2%;   Score 511.5;   DB 22;   Length 128;
Best Local Similarity   80.5%;   Pred. No. 3.6e-44;
Matches  107;  Conservative   7;  Mismatches  12;  Indels   7;  Gaps   3;

Qy    1 EVQLLESGVESGGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
          ||||| ::|:||||||||||||||||||||||||||:|||||||||||:::||::
Db    1 EVQL----VESGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYSISSSS 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRY--SNFLRWVRSDGM 118
          |||| | ||||||||||||||||||||||||||:|||:|   | |
Db   57 YIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDNYYDSSGSLRRYY-GM 115

Qy  119 DVWGQGTTVIVSS 131
          |||||| | |||
Db  116 DVWGQGTLVTVSS 128
```

```
; GENERAL INFORMATION:
;   APPLICANT: Human Genome Sciences, Inc.
;   TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;   FILE REFERENCE: PF523PCT
;   CURRENT APPLICATION NUMBER: PCT/US01/19110
;   CURRENT FILING DATE: 2001-06-15
;   PRIOR APPLICATION NUMBER: 60/212,210
;   PRIOR FILING DATE: 2000-06-15
;   PRIOR APPLICATION NUMBER: 60/240,816
;   PRIOR FILING DATE: 2000-10-17
;   PRIOR APPLICATION NUMBER: 60/276,248
;   PRIOR FILING DATE: 2001-03-16
;   PRIOR APPLICATION NUMBER: 60/277,379
;   PRIOR FILING DATE: 2001-03-21
;   PRIOR APPLICATION NUMBER: 60/293,499
;   PRIOR FILING DATE: 2001-05-25
;   NUMBER OF SEQ ID NOS: 3239
;   SOFTWARE: Patentin Ver. 2.0
;   SEQ ID NO 1318
;     LENGTH: 256
;     TYPE: PRT
;     ORGANISM: Homo sapiens
PCT-US01-19110-1318

Query Match             74.2%;   Score 511.5;   DB 1;   Length 256;
Best Local Similarity   78.2%;   Pred. No. 8.2e-44;
Matches  104;  Conservative  11;  Mismatches  11;  Indels   7;  Gaps   3;

Qy    1 EVQLLESGVESGGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
          |||||  :|:||||||||||||||||||||||||||:|||||||||||:::||::
Db    1 EVQL----VQSGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYSISSSS 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARD-SRYSNFLRWVRSD--G 117
          |||| | |||||||||||||||||||||||||:|||:|  | | |
Db   57 YIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLGSFYDILTALRLENYG 116

Qy  118 MDVWGQGTTVIVS 130
          ||||| | | |||
Db  117 MDVWGKGTLVTVS 129
```

```
RESULT 12
PCT-US02-36496-1318
; Sequence 1318, Application PC/TUS0236496
; GENERAL INFORMATION:
;   APPLICANT: Human Genome Sciences, Inc.
;   TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;   FILE REFERENCE: PF523PCT2
;   CURRENT APPLICATION NUMBER: PCT/US02/36496
;   CURRENT FILING DATE: 2002-11-14
;   PRIOR APPLICATION NUMBER: 60/331,469
;   PRIOR FILING DATE: 2001-11-16
;   PRIOR APPLICATION NUMBER: 60/340,817
;   PRIOR FILING DATE: 2001-12-19
;   SEQ ID NO 1318
;     LENGTH: 256
;     TYPE: PRT
;     ORGANISM: Homo sapiens
PCT-US02-36496-1318

Query Match             74.2%;   Score 511.5;   DB 1;   Length 256;
Best Local Similarity   78.2%;   Pred. No. 8.2e-44;
Matches  104;  Conservative  11;  Mismatches  11;  Indels   7;  Gaps   3;

Qy    1 EVQLLESGVESGGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
          |||||  :|:||||||||||||||||||||||||||:|||||||||||:::||::
Db    1 EVQL----VQSGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYSISSSS 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARD-SRYSNFLRWVRSD--G 117
          |||| | |||||||||||||||||||||||||:|||:|  | | |
Db   57 YIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLGSFYDILTALRLENYG 116

Qy  118 MDVWGQGTTVIVS 130
          ||||| | | |||
Db  117 MDVWGKGTLVTVS 129
```

```
RESULT 11
PCT-US01-19110-1318
; Sequence 1318, Application PC/TUS0119110
```

Qy 118 MDVWGQGTTVIVS 130
         |||||:|| | ||
Db 117 MDVWGKGTLVTVS 129

RESULT 13
US-09-880-748-1318
Sequence 1318, Application US/09880748
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1318
LENGTH: 256
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1318

Query Match   74.28;   Score 511.5; DB 23; Length 256;
Best Local Similarity   78.2%;   Pred. No. 8.2e-44;
Matches 104; Conservative 11; Mismatches 11; Indels 7; Gaps 3;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
         |||| :|||||||||||||||||||||||||||||||||:|||| |:||| ||||||:||:
Db   1 EVQL---VQSGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISNSNT 56

Qy 61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARD-SRYSNFLRWVRSD--G 117
         ||||| :||||||||||||||||||||||||||:|||||||| :| | | :| |
Db 57 YIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLGSFYDILTALRLENYG 116

Qy 118 MDVWGQGTTVIVS 130
         |||||:|| | ||
Db 117 MDVWGKGTLVTVS 129

RESULT 14
US-10-293-418-1318
Sequence 1318, Application US/10293418
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1318
LENGTH: 256
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-1318

Query Match   74.28;   Score 511.5; DB 28; Length 256;
Best Local Similarity   78.2%;   Pred. No. 8.2e-44;
Matches 104; Conservative 11; Mismatches 11; Indels 7; Gaps 3;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
Db   1 EVQL---VQSGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISNSNT 56

Qy 61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARD-SRYSNFLRWVRSD--G 117
Db 57 YIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLGSFYDILTALRLENYG 116

Qy 118 MDVWGQGTTVIVS 130
Db 117 MDVWGKGTLVTVS 129

RESULT 15
PCT-US01-19110-913
Sequence 913, Application PCT/US0119110
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523PCT
CURRENT APPLICATION NUMBER: PCT/US01/19110
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 913
LENGTH: 248
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US01-19110-913

Query Match   73.9%;   Score 509; DB 1; Length 248;
Best Local Similarity   78.6%;   Pred. No. 1.4e-43;
Matches 103; Conservative 8; Mismatches 14; Indels 6; Gaps 2;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
Db   1 EVQL---VESGGGLVQPGGSLRLSCAAFGFTFSSYSMNWVRQRQAPGKGLEWVSSISNRGS 56

Qy 61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
Db 57 YIYYADSVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYCAREGR--DILTGVYYGLDV 114

Qy 121 WGQGTTVIVSS 131
Db 115 WGQGTLVTVSS 125

Search completed: September 24, 2003, 06:36:26
Job time : 343 secs

OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: September 24, 2003, 06:27:35 ; Search time 90 Seconds
                (without alignments)
                37.475 Million cell updates/sec

Title: US-09-848-798A-28
Perfect score: 689
Sequence: 1 EVQLLESGVESGGGLVKPGG............WVRSDGMDVWGQGTTVIVSS 131

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 120229 seqs, 25746487 residues

Total number of hits satisfying chosen parameters: 120229

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :
        Pending_Patents_AA_New:*
        1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
        2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
        3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
        4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
        5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
        6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
        7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	507.5	73.7	245	5	US-09-138-091A-76	Sequence 76, Appl
2	507	73.6	123	1	PCT-US03-21304-56	Sequence 56, Appl
3	488	70.8	249	1	PCT-US03-25457-53	Sequence 53, Appl
4	479.5	69.6	245	5	US-09-138-091A-73	Sequence 73, Appl
5	477.5	69.3	245	6	US-10-645-215-6	Sequence 6, Appli
6	475	68.9	247	1	PCT-US03-23826-44	Sequence 44, Appl
7	463	67.2	143	6	US-10-469-304-17	Sequence 17, Appl
8	463	67.2	474	1	PCT-US02-26584-3	Sequence 3, Appli
9	460	66.8	113	5	US-09-723-752B-11	Sequence 11, Appl
10	458	66.5	131	1	PCT-US03-15937-53	Sequence 53, Appl
11	457.5	66.4	124	6	US-10-031-722A-2	Sequence 2, Appli
12	454.5	66.0	223	1	PCT-US03-26779-96	Sequence 46, Appl
13	454.5	66.0	223	1	PCT-US03-26744-90	Sequence 90, Appl
14	454.5	66.0	223	7	US-60-485-404-46	Sequence 46, App
15	453	65.7	145	1	PCT-US03-26232-146	Sequence 146, App
16	452	65.6	121	1	PCT-US03-22566-2	Sequence 2, Appli
17	450	65.3	119	1	PCT-US03-21590-6	Sequence 6, Appli
18	449	65.2	228	1	PCT-US03-26779-99	Sequence 99, Appl
19	449	65.2	228	1	PCT-US03-26744-93	Sequence 93, Appl
20	449	65.2	228	7	US-60-485-404-49	Sequence 49, Appl
21	446	64.7	117	1	PCT-US03-25161-18	Sequence 18, Appl
22	441	64.0	119	1	PCT-US03-11113-10	Sequence 10, Appl
23	441	64.0	119	1	PCT-US03-11113-16	Sequence 16, Appl
24	439.5	63.8	245	5	US-09-138-091A-74	Sequence 74, Appl
25	438.5	63.6	116	1	PCT-US03-10749A-14	Sequence 14, Appl
26	438.5	63.6	242	5	US-09-538-038A-2351	Sequence 2351, Ap
27	438.5	63.6	446	1	PCT-US03-10749A-38	Sequence 38, Appl
28	437	63.4	117	1	PCT-US03-21304-57	Sequence 57, Appl
29	435	63.1	117	1	PCT-US03-21304-59	Sequence 59, Appl
30	435	63.1	239	5	US-09-538-038A-2353	Sequence 2353, Ap
31	434	63.0	117	5	PCT-US03-21304-58	Sequence 58, Appl
32	433.5	62.9	122	6	US-10-031-722A-6	Sequence 6, Appli
33	432	62.7	117	6	US-10-257-864A-99	Sequence 99, Appl
34	432	62.7	136	6	US-10-257-864A-102	Sequence 102, App
35	432	62.7	244	5	US-09-138-091A-75	Sequence 75, Appl
36	432	62.7	266	6	US-10-257-864A-108	Sequence 108, App
37	431	62.6	123	1	PCT-US03-19333-38	Sequence 38, Appl
38	431	62.6	246	1	PCT-US03-19333-24	Sequence 24, Appl
39	430.5	62.5	124	5	US-09-610-551B-63	Sequence 63, Appl
40	430	62.4	121	1	PCT-US03-22566-10	Sequence 10, Appl
41	429	62.3	246	1	PCT-US03-19333-23	Sequence 23, Appl
42	427.5	62.0	460	1	PCT-US03-23735-5	Sequence 5, Appli
43	426.5	61.9	120	1	PCT-US02-34154-7	Sequence 7, Appli
44	426.5	61.9	120	6	US-10-456-092A-7	Sequence 7, Appli
45	426.5	61.9	122	6	US-10-031-722A-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-138-091A-76

Sequence 76, Application US/09138091A
GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: 9491-013-27
; CURRENT APPLICATION NUMBER: US/09/138,091A
; CURRENT FILING DATE: 1998-08-21
; PRIOR APPLICATION NUMBER: US 60/056,736
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: single chain antibody (scFv) fragments
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 208
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-138-091A-76

Query Match   73.7%; Score 507.5; DB 5; Length 245;
Best Local Similarity 77.9%; Pred. No. 9.6e-35;
Matches 102; Conservative 9; Mismatches 7; Indels 13; Gaps 2;

Qy   1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT   60
         ||||||||:|||||||||||||||||||||||||||||:|:|||||:||||||||:|||:
Db   3 QVQL----VESGGGLVKPGGSLRLSCAASGFTFSSHNMNWVRQAPGKGLEWVSSISSSS   58

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
         ||||||:||||||||||||||||||||||||||:|||||||||| | ||||
Db   59 YIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDR-------GSIGMDV 109

Qy 121 WGQGTTVIVSS 131
         ||:||| ||||
Db 110 WGRGTLVTVSS 120

RESULT 2
PCT-US03-21304-56
; Sequence 56, Application PC/TUS0321304
; GENERAL INFORMATION:

```
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
; TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS AND INHIBITORS THEREOF
; FILE REFERENCE: 053893-5050WO
; CURRENT FILING DATE: 2003-07-03
; CURRENT APPLICATION NUMBER: PCT/US03/21304
; PRIOR APPLICATION NUMBER: 60/394,356
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/411,694
; PRIOR FILING DATE: 2003-09-18
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 56
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US03-21304-56

Query Match            73.6%;  Score 507;  DB 1;  Length 123;
Best Local Similarity  79.5%;  Pred. No 5.8e-35;
Matches 105;  Conservative  8;  Mismatches  9;  Indels  10;  Gaps  4;

Qy      1 EVQLLESGVESGGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
          |||| |  ||||||||||||||||||||||||||||||||:||||:||||||||| | |::
Db      1 EVQL---VESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSS 56

Qy     61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGM-D 119
          ||||||:||||||||||||||||||||||||||:|||||||||:   :|:|  : |: |
Db     57 YIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARD--HPNY---YDSSGLFD 111

Qy    120 VWGQGTTVTVSS 131
          :|||||| ||||
Db    112 YWGQGTLVTVSS 123
```

```
RESULT 3
PCT-US03-25457-53
Sequence 53, Application PC/TUS03325457
GENERAL INFORMATION:
   APPLICANT: Human Genome Sciences, Inc.
   TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
   TITLE OF INVENTION: Receptors
   FILE REFERENCE: PF550PCT2
   CURRENT APPLICATION NUMBER: PCT/US03/25457
   CURRENT FILING DATE: 2003-08-15
   PRIOR APPLICATION NUMBER: 60/468,050
   PRIOR FILING DATE: 2003-05-06
   PRIOR APPLICATION NUMBER: 60/425,730
   PRIOR FILING DATE: 2002-11-13
   PRIOR APPLICATION NUMBER: 60/403,382
   PRIOR FILING DATE: 2002-08-15
   NUMBER OF SEQ ID NOS: 70
SEQ ID NO 53
LENGTH: 249
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
   OTHER INFORMATION: T1006F07 scFv
PCT-US03-25457-53

Query Match            70.8%;  Score 488;  DB 1;  Length 249;
Best Local Similarity  75.8%;  Pred. No 3.8e-33;
Matches 100;  Conservative  9;  Mismatches 15;  Indels  8;  Gaps  3;

Qy      1 EVQLLESGVESGGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
          |||| |  ||||||||||||||||||||||||||||||||:||||:||||||||| | |::
Db      1 EVQLL----ESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGG 56

Qy     61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVR-SDGMD 119
          |||||:||||||||||||:|||||||||||||||:||||||||:  :|:|||| : | |
Db     57 STYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARE---PSFQQWGHYSYGMD 113

Qy    120 VWGQGTTVTVSS 131
          :|||||| ||||
Db    114 VWGQGTMVTVSS 125
```

```
RESULT 4
US-09-138-091A-73
Sequence 73, Application US/09138091A
GENERAL INFORMATION:
   APPLICANT: Adams, Camellia W.
   APPLICANT: Carter, Paul J.
   APPLICANT: Fendly, Brian M.
   APPLICANT: Gurney, Austin L.
   TITLE OF INVENTION: Agonist Antibodies
   FILE REFERENCE: 9491-013-27
   CURRENT APPLICATION NUMBER: US/09/138,091A
   CURRENT FILING DATE: 1998-08-21
   PRIOR APPLICATION NUMBER: US 60/056,736
   PRIOR FILING DATE: 1997-08-22
   NUMBER OF SEQ ID NOS: 77
   SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 73
LENGTH: 245
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
   OTHER INFORMATION: single chain antibody (scFv) fragments
US-09-138-091A-73

Query Match            69.6%;  Score 479.5;  DB 5;  Length 245;
Best Local Similarity  72.5%;  Pred. No 1.8e-32;
Matches 95;  Conservative  8;  Mismatches 15;  Indels  13;  Gaps  2;

Qy      1 EVQLLESGVESGGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT 60
          |||| |  :|||||||||||||||||||||||||  :| |:||||||||||||| |   :|
Db      3 EVQL---VQSGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGS 58

Qy     61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
          ||||||:||||||||||||:|||:||||||||||:||||||            |:||| |
Db     59 TIYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCA----------RWSGEDAFDI 109

Qy    121 WGQGTTVTVSS 131
          ||||| ||||
Db    110 WGQGTMVTVSS 120
```

```
RESULT 5
US-10-645-215-6
Sequence 6, Application US/10645215
GENERAL INFORMATION:
   APPLICANT: Adolf, Guenther
   APPLICANT: Baum, Anke
   APPLICANT: Heider, Karl-Heinz
   TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
   TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
   TITLE OF INVENTION: Chemotherapeutic Agents
   FILE REFERENCE: 1/1383
   CURRENT APPLICATION NUMBER: US/10/645,215
   CURRENT FILING DATE: 2003-08-21
   PRIOR APPLICATION NUMBER: EP 02 018 686.2
   PRIOR FILING DATE: August 21, 2002
   PRIOR APPLICATION NUMBER: US 60/405,956
   PRIOR FILING DATE: August 26, 2002
   NUMBER OF SEQ ID NOS: 9
   SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 444
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
   OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain
US-10-645-215-6

Query Match            69.3%;  Score 477.5;  DB 6;  Length 444;
```

```
Best Local Similarity 72.5%;   Pred. No. 4.4e-32;
Matches 95; Conservative 7; Mismatches 12; Indels 17; Gaps 2;

Qy    1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHHVRQGPGKGLEWVSSISNSNT 60
          ||||     |||||||||||||||||||||||| | ||||| || || |||||| |
Db    1 EVQL----VESGGGLVKPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVSTISSGGS 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
          | | |  |||||||||||||||||||||||||| ||||||||
Db   57 YTYYLDSIKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR-----------QGLDY 103

Qy  121 WGQGTTVIVSS 131
          | ||| | |||
Db  104 WGRGTLVTVSS 114
```

RESULT 6
PCT-US03-23826-44
Sequence 44, Application PCT/US0323826
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Antibodies Against C3a Receptor
FILE REFERENCE: PF588PCT
CURRENT APPLICATION NUMBER: PCT/US03/23826
CURRENT FILING DATE: 2003-07-31
PRIOR APPLICATION NUMBER: 60/400,057
PRIOR FILING DATE: 2002-08-02
NUMBER OF SEQ ID NOS: 50
SEQ ID NO 44
LENGTH: 247
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: D185G07 scFv

PCT-US03-23826-44

```
Query Match      68.9%;  Score 475;  DB 1;  Length 247;
Best Local Similarity 72.3%;  Pred. No. 4.3e-32;
Matches 94; Conservative 10; Mismatches 16; Indels 10; Gaps 2;

Qy    1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHHVRQGPGKGLEWVSSISNSNT 60
          ||||     |||||||||||||||||||||||:|| | ||||| || || |:||::
Db    1 QVQL----VESGGGLVKPGGSLRLSCAASGFTFSDYMSWIRQAPGKGLEWVSYISSSS 56

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
          |  | || :||||||||||||||||||||||||| | |||||| :
Db   57 YTNYADSVKGRFFISRDNAKNSLYLQMNSLRAEDTAVYYCARGPDYDSY-----DAFDI 110

Qy  121 WGQGTTVIVSS 130
          || ||| | ||
Db  111 WGKGTLVTVSS 120
```

RESULT 7
US-10-469-304-17
Sequence 17, Application US/10469304
GENERAL INFORMATION:
APPLICANT: KIRIN BEER KABUSHIKI KAISHA
TITLE OF INVENTION: Anti HLA-DR antibody
FILE REFERENCE: PH-1646-PCT
CURRENT APPLICATION NUMBER: US/10/469,304
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: JP2001/317054
PRIOR FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 143
TYPE: PRT
ORGANISM: Homo sapiens
US-10-469-304-17

Query Match   67.2%; Score 463; DB 6; Length 143;

```
Best Local Similarity 71.8%;  Pred. No. 2.5e-31;
Matches 94; Conservative 8; Mismatches 21; Indels 8; Gaps 2;

Qy    1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHHVRQGPGKGLEWVSSISNSNT 60
          ||||||    |||||||||||||||||||||||||| | |||| || |||||| |
Db   20 EVQLL----ESGGGLVKPGGSLRLSCAASGFTFSSYAMTWVRQAPGKGLEWVSGISGGGD 75

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
          | | || ||||||||||||| |||||||||||| |||||||  :  :
Db   76 STYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDHGSGSYPY----WFDY 131

Qy  121 WGQGTTVIVSS 131
          ||||| | |||
Db  132 WGQGTLVTVSS 142
```

RESULT 8
PCT-US02-26584-3
Sequence 3, Application PCT/US0226584
GENERAL INFORMATION:
APPLICANT: HOOPER, Craig
APPLICANT: DIETZSCHOLD, Bernhard
TITLE OF INVENTION: Recombinant Antibodies, and Compositions
TITLE OF INVENTION: and Methods for Making Them
FILE REFERENCE: 8321-110 PC
CURRENT APPLICATION NUMBER: PCT/US02/26584
CURRENT FILING DATE: 2002-08-21
PRIOR APPLICATION NUMBER: US 60/314,023
PRIOR FILING DATE: 2001-08-21
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 474
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-26584-3

```
Query Match      94%;  Score 463;  DB 1;  Length 474;
Best Local Similarity 71.8%;  Pred. No. 7.1e-31;
Matches 94; Conservative 11; Mismatches 20; Indels 6; Gaps 2;

Qy    1 EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHHVRQGPGKGLEWVSSISNSNT 60
          |||||    |||||| |||||||||||||||||||:| | |||| || |||||| |
Db   20 EVQLL----ESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISASGH 75

Qy   61 YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
          | | || ||||||||||||| |||||||||||| |||||||:  :    :
Db   76 STYLADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDREVTMIV--VLNGGFDY 133

Qy  121 WGQGTTVIVSS 131
          ||||| | |||
Db  134 WGQGTRVTVSS 144
```

RESULT 9
US-09-723-752B-11
Sequence 11, Application US/0972375ZB
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
          Wells, James A.
          Presta, Leonard G.
          Lowman, Henry B.
          Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:

```
;      MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/723,752B
;      FILING DATE: 27-Nov-2000
;      CLASSIFICATION: <Unknown>
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 08/908469
;      FILING DATE: 06-AUG-1997
;      APPLICATION NUMBER: 08/833504
;      FILING DATE: 07-APR-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME: Cui, Steven X.
;      REGISTRATION NUMBER: 44,637
;      REFERENCE/DOCKET NUMBER: P1093P1D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 650/225-8674
;      TELEFAX: 650/952-9881
;    INFORMATION FOR SEQ ID NO: 11:
;      SEQUENCE CHARACTERISTICS:
;        LENGTH: 113 amino acids
;        TYPE: Amino Acid
;        TOPOLOGY: Linear
;      SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-723-752B-11
```

```
RESULT 10
PCT-US03-15937-53
; Sequence 53, Application PC/TUS0315937
; GENERAL INFORMATION:
; APPLICANT: Hematech, LLC et al.
; APPLICANT:
; TITLE OF INVENTION: Transgenic Ungulates Capable of Human
; TITLE OF INVENTION: Antibody Production
; FILE REFERENCE: 50195/012W02
; CURRENT APPLICATION NUMBER: PCT/US03/15937
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/381,531
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/425,056
; PRIOR FILING DATE: 2002-11-08
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Bovine
PCT-US03-15937-53

  Query Match           66.5%;  Score 458;   DB 1;   Length 131;
  Best Local Similarity 74.8%;  Pred. No. 6e-31;
  Matches  89;  Conservative   6;  Mismatches 14;  Indels 10;  Gaps  1;

Qy  13 GGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNTYIYADAVKGRF  72
        |||||||||||||||||||||||||||||| ||| |:|| ||||||::|||| ||:||
```

```
Qy   1 EVQLLESGVESGGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSYISSSGSTIYADSVKGRF  60
         ||||    ||||:|||||||||||||||   |||||||||
Db   1 EVQL----VESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISGDG  56

Qy  61 YIYIADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
         ||:|| |||||||||||||||||||||||||||||||||||:|:|||||||||
Db  57 STYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR----------GFDY 102

Qy 121 WGQGTTVIVSS 131
         ||||| | |||
Db 103 WGQGTLVTVSS 113
```

```
Db   1 GGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYADSVKGRF  60
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Qy  73 TISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDVWGQGTTVIVSS 131
        |||||||||||||||||||| |||||||||                  :|||| || |||
Db  61 TISRDNAKNSLYLQMNSLRAEDTAVYYCAR-----------ITGDAFFDIWGQGTMVTVSS 109
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```
RESULT 11
US-10-031-722A-2
; Sequence 2, Application US/10031722A
; GENERAL INFORMATION:
; APPLICANT: Medarex, Inc.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HER2/NEU
; FILE REFERENCE: MXI-160PC
; CURRENT APPLICATION NUMBER: US/10/031,722A
; CURRENT FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: USSN 60/146,313
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: USSN 60/188,539
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-031-722A-2

  Query Match           66.4%;  Score 457.5;   DB 6;   Length 124;
  Best Local Similarity 71.0%;  Pred. No. 6.2e-31;
  Matches  93;  Conservative 10;  Mismatches 21;  Indels  7;  Gaps  2;
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```
Qy   1 EVQLLESGVESGGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT  60
         ||||    ||||:|||||||||||||||:|| |||| || :|| |||| ||||||::||
Db   1 EVQLL---ESGGGLVQPGGSLRLSCAASGFTFSSYAMTWVRQAPGKGLEWVSAISGSGY  56

Qy  61 YIYIADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV 120
         ||:||||||||||||||||||||||||||||| |||||||| : : |
Db  57 STYYADSEKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKGFQYGSGSYYTH---FDY 113

Qy 121 WGQGTTVIVSS 131
         ||||| | |||
Db 114 WGQGTLVTVSS 124
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```
RESULT 12
PCT-US03-26779-46
; Sequence 46, Application PC/TUS0326779
; GENERAL INFORMATION:
; APPLICANT: Prior, Christopher P.
; APPLICANT: Turner, Andrew J.
; APPLICANT: Sadeghi, Homayoun
; TITLE OF INVENTION: Transferrin Fusion Protein Libraries
; FILE REFERENCE: 054710-5007-WO
; CURRENT APPLICATION NUMBER: PCT/US03/26779
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 10/384,060
; PRIOR FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 60/485,404
; PRIOR FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 46
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: VH region of anti-TNF-alpha antibody, Gen Bank No. BAB18250
PCT-US03-26779-46
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RESULT 13
PCT-US03-26744-90
Sequence 90, Application PC/TUS0326744
GENERAL INFORMATION:
APPLICANT: SADEGHI, Homayoun
APPLICANT: PRIOR, Christopher P.
APPLICANT: TURNER, Andrew
TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
FILE REFERENCE: 54710-5004-WO
CURRENT APPLICATION NUMBER: PCT/US03/26744
CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: US 60/406,977
PRIOR FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 10/384,060
PRIOR FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 99
SOFTWARE: Patentin version 3.2
SEQ ID NO 90
LENGTH: 223
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: VH region of anti-TNF-alpha antibody, Gen Bank No. BAB18250
PCT-US03-26744-90

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Query Match     66.0%;    Score 454.5;   DB 1;   Length 223;
Best Local Similarity    70.2%;   Pred. No. 1.8e-30;
Matches  92;  Conservative  10;  Mismatches  16;  Indels  13;  Gaps  2;

Qy    1  EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT  60
         :|||| |:|:|:|| |||||||||||||||||| ||||| |||||||||:|||||| :
Db    1  QVQLL---ESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGS  56

Qy   61  YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV  120
         ||||:|||||||||||||:||||||:|||||||||:||||||| |::|| :
Db   57  NKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDSGDLAF-------DI  107

Qy  121  WGQGTTVIVSS  131
         |||||| | ||
Db  108  WGQGTMVTVSS  118
```

RESULT 14
US-60-485-404-46
Sequence 46, Application US/60485404
GENERAL INFORMATION:
APPLICANT: Prior, Christopher P.
APPLICANT: Turner, Andrew J.
APPLICANT: Sadeghi, Homayoun
TITLE OF INVENTION: Transferrin Fusion Protein Libraries
FILE REFERENCE: 05710-5007-PR
CURRENT APPLICATION NUMBER: US/60/485,404
CURRENT FILING DATE: 2003-07-09
PRIOR APPLICATION NUMBER: US 10/231,494
PRIOR FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 60/406,997
PRIOR FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 10/384,060
PRIOR FILING DATE: 2003-03-10
PRIOR APPLICATION NUMBER: US 60/460,829
PRIOR FILING DATE: 2003-04-08
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 46
LENGTH: 223
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: VH region of anti-TNF-alpha antibody, Gen Bank No. BAB18250
US-60-485-404-46

```
Query Match     66.0%;    Score 454.5;   DB 7;   Length 223;
Best Local Similarity    70.2%;   Pred. No. 1.8e-30;
Matches  92;  Conservative  10;  Mismatches  16;  Indels  13;  Gaps  2;

Qy    1  EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNT  60
         :|||| |:|:|:|| |||||||||||||||||| ||||| |||||||||:|||||| :
Db    1  QVQLL---ESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGS  56

Qy   61  YIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDV  120
         ||||:|||||||||||||:||||||:|||||||||:||||||| |::|| :
Db   57  NKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDSGDLAF-------DI  107

Qy  121  WGQGTTVIVSS  131
         |||||| | ||
Db  108  WGQGTMVTVSS  118
```

RESULT 15
PCT-US03-26232-146
Sequence 146, Application PC/TUS0326232
GENERAL INFORMATION:
APPLICANT: ABGENIX, INC.
APPLICANT: GUDAS, Jean M.
APPLICANT: HAAK-FRENDSCHO, Mary
APPLICANT: FOORD, Orit
APPLICANT: LIANG, Meina L.
APPLICANT: AHLUWALIA, Kiran
APPLICANT: BHAKTA, Sunil
TITLE OF INVENTION: ANTIBODIES DIRECTED TO MONOCYTE CHEMO-ATTRACTANT PROTEIN-1 (MCP-1) AND USES THEREOF
FILE REFERENCE: ABGENIX.091VPC
CURRENT APPLICATION NUMBER: PCT/US03/26232
CURRENT FILING DATE: 2003-08-19
PRIOR APPLICATION NUMBER: US 60/404,802
PRIOR FILING DATE: 2002-08-19
NUMBER OF SEQ ID NOS: 149
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 146
LENGTH: 145
TYPE: PRT
ORGANISM: Homosapien
PCT-US03-26232-146

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Query Match     65.7%;    Score 453;   DB 1;   Length 145;
Best Local Similarity    73.8%;   Pred. No. 1.7e-30;
Matches  90;  Conservative  10;  Mismatches  16;  Indels  6;  Gaps  2;

Qy   10  ESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQGPGKGLEWVSSISNSNTYIYYADAVK  69
         :|||| |:|| ||||||||||||||||| |||||||:||||||||: | |||||:||
Db    2  QSGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGNNKYYADSVK  61

Qy   70  GRFTISRDNAKNSLYLQMNSLRAEHTAVYYCARDSRYSNFLRWVRSDGMDVWGQGTTVIV  129
         ||||||||:.:|| |||||||||||:|||||||||||   :||||:   ||:|||||||:|
Db   62  GRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARDS--SSYYY----GMDVWGQGTTVTV  115

Qy  130  SS  131
```

Db   116 SS 117

Search completed: September 24, 2003, 06:38:05
Job time : 90 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2003, 22:39:53 ; Search time 2208 Seconds
(without alignments)
7281.469 Million cell updates/sec

Title: US-09-848-798A-97
Perfect score: 393
Sequence: 1 gaggtgcagctgctcgagtc.........ccacggtcatcgtctccctca 393

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 60 summaries

Database : GenEmbl:*
          GenEmbl:
          1: gb_ba:*
          2: gb_htg:*
          3: gb_in:*
          4: gb_om:*
          5: gb_ov:*
          6: gb_pat:*
          7: gb_ph:*
          8: gb_pl:*
          9: gb_pr:*
          10: gb_ro:*
          11: gb_sts:*
          12: gb_sy:*
          13: gb_un:*
          14: gb_vi:*
          15: em_ba:*
          16: em_fun:*
          17: em_hum:*
          18: em_in:*
          19: em_mu:*
          20: em_om:*
          21: em_or:*
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          25: em_pl:*
          26: em_ro:*
          27: em_sts:*
          28: em_un:*
          29: em_vi:*
          30: em_htg_hum:*
          31: em_htg_inv:*
          32: em_htg_other:*
          33: em_htg_mus:*
          34: em_htg_pln:*
          35: em_htg_rod:*
          36: em_htg_mam:*
          37: em_htg_vrt:*
          38: em_sy:*
          39: em_htgo_hum:*
          40: em_htgo_mus:*
          41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	393	100.0	393	6	AR160968	AR160968 Sequence
2	393	100.0	393	12	AF044446	AF044446 Synthetic
3	363.6	92.5	381	12	AR160967	AR160967 Sequence
4	363.6	92.5	381	6	AF044445	AF044445 Synthetic
5	306	77.9	435	9	HSA234196	AJ234196 Homo sapi
6	296.2	75.4	396	9	HSA519295	AJ519295 Homo sapi
7	294	74.8	378	9	AB066972	AB066972 Homo sapi
8	293.6	74.7	435	9	AF062202	AF062202 Homo sapi
9	293.2	74.6	402	9	HSA389193	AJ389193 Homo sapi
10	291.6	74.2	378	9	HSA519292	AJ519292 Homo sapi
11	288.2	73.3	384	9	HSU77374	U77374 Homo sapien
12	286.6	72.9	385	9	HUMVH3H	D83682 Human mRNA
13	284.8	72.5	438	9	AF032350	AF032350 Homo sapi
14	284	72.3	372	9	AF170095	AF170095 Homo sapi
15	283	72.0	387	9	HSA555251	AF555251 Homo sapi
16	279.6	71.1	375	9	AF174081	AF174081 Homo sapi
17	278.8	70.9	389	9	HSY12442	Y12442 H.sapiens I
18	278.6	70.9	384	9	AF466106	AF466106 Homo sapi
19	278.6	70.9	384	9	AF466107	AF466107 Homo sapi
20	278.6	70.9	441	9	HSROU221	HSROU221 Homo sapi
21	278	70.7	429	9	AY190818	AY190818 Homo sapi
22	277.2	70.5	378	9	HSA271554	AJ271554 Homo sapi
23	277.2	70.5	381	6	U00501	U00501 Human immun
24	277.2	70.5	524	9	HUMIGHZI	HUMIGHZI Human immun
25	276	70.2	432	9	AY033254	AY033254 Homo sapi
26	275.4	70.1	363	9	HUMIGH3AA	HUMIGH3AA Human immun
27	274.8	69.9	519	6	L08082	L08082 Human (clon
28	274.8	69.9	372	9	HUMVH3L	D83686 Human mRNA
29	274.4	69.9	357	9	HSU77372	U77372 Homo sapien
30	274.2	69.8	357	9	U00572	U00572 Human immun
31	274	69.7	387	9	AB063691	AB063691 Homo sapi
32	273.2	69.5	392	9	HSU80144	U80144 Human immun
33	273	69.5	488	9	HSIG488	X61014 Human Immun
34	272.2	69.3	339	9	HSMVH0007	HSMVH0007 Human immun
35	272.2	69.3	519	6	BD013945	BD013945 Humanized
36	272.2	69.3	519	9	HUMIGH321X	HUMIGH321x Human immun
37	272.2	69.3	200000	2	AB019439	AB019439 Human immun
38	272.2	69.3	227353	2	AC141259	AC141259 Sequence
39	271.8	69.1	375	2	AX061434	AX061434 Sequence
40	271.6	69.1	372	9	HSU95238	U95238 Human clone
41	271.6	69.1	388	9	HSA389186	AJ389186 Homo sapi
42	271.6	69.1	458	9	HSE5432	HSE5432 Homo sapi
43	271.6	69.0	358	9	HSA556823	AJ556823 H.sapiens r
44	271.4	69.0	352	9	HSA556824	AJ556824 H.sapiens r
45	271.2	69.0	712	12	HSRIGHVDJ	HSRIGHVDJ H.sapiens i
46	271.2	69.0	819	9	HSA225092	AJ225092 Synthetic
47	271.2	69.0	321	9	HSA406683	HSA406683 Homo sapi
48	271	68.9	378	9	AF004319	AF004319 Homo sapi
49	270.6	68.9	60962	2	AC103742	AC103742 Homo sapi
50	270.4	68.8	357	9	HSIG486	L19904 Human clone
51	270.2	68.8	486	9	HSIGDP77	X61011 Human Immun
52	270.2	68.8	294	9	HSA406723	HSIGDP77 Homo sapi
53	270.2	68.8	336	9	HSIHCVD3	Z14073 H.sapiens g
54	270.2	68.8	339	9	HSA556832	AJ406723 H.sapiens m
55	270	68.8	346	9	BC024289	X99354 H.sapiens m
56	270	68.7	1630	9	Z37313	HSA556832 Homo sapi
57	269.6	68.6	378	9	HSIGVHC25	BC024289 Homo sapi
58	269.6	68.6	393	9	HSJ001171	Z37313 H.sapiens r
59	269.6	68.6	423	9	AF062121	HSIGVHC25 Homo sapi
60	269.2	68.5	378	9	HSA239390	HSJ001171 Homo sapi

Pred. No. is the number of results predicted by chance to have a

ALIGNMENTS

RESULT 1

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LOCUS       AR160968       393 bp    DNA      linear    PAT 17-OCT-2001
DEFINITION  Sequence 97 from patent US 6255455.
ACCESSION   AR160968
VERSION     AR160968.1  GI:16226171
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 393)
  AUTHORS   Siegel,D.L.
  TITLE     Rh(D)-binding proteins and magnetically activated cell sorting
            method for production thereof
  JOURNAL   Patent: US 6255455-A 97 03-JUL-2001;
FEATURES             Location/Qualifiers
     source          1..393
                     /organism="unknown"
BASE COUNT       88 a     99 c    120 g    86 t
ORIGIN
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Query Match       100.0%;  Score 393;  DB 6;  Length 393;
Best Local Similarity   100.0%;
Matches 393;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTCAAGCCTGGGGGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTCAAGCCTGGGGGG 60

Qy   61 TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATAGCCATGCACTGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATAGCCATGCACTGG 120

Qy  121 GTCCGCCAGGGTCCAGGGAAGGGGCTGGAGTGGGTCTCATCCATTAGTAATAGTAATACT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GTCCGCCAGGGTCCAGGGAAGGGGCTGGAGTGGGTCTCATCCATTAGTAATAGTAATACT 180

Qy  181 TACATATACTACGCAGACGCAGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 TACATATACTACGCAGACGCAGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAG 240

Qy  241 AACTCACTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTACTACTGT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 AACTCACTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTACTACTGT 300

Qy  301 GCGAGAGATTCTAGATACTACAGTAATTTCCTCCGTTGGGTTCGGAGCGACGGTATGGACGTC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 GCGAGAGATTCTAGATACTACAGTAATTTCCTCCGTTGGGTTCGGAGCGACGGTATGGACGTC 360

Qy  361 TGGGGCCAAGGGACCACACGGTCATCGTCTCCTCA 393
          ||||||||||||||||||||||||||||||||||||
Db  361 TGGGGCCAAGGGACCACACGGTCATCGTCTCCTCA 393
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RESULT 2

```
LOCUS       AF044446       393 bp    mRNA     linear    SYN 31-OCT-2001
DEFINITION  Synthetic construct from Homo sapiens clone E03 anti-Rh(D) antibody
            VH segment mRNA, partial cds.
ACCESSION   AF044446
VERSION     AF044446.1  GI:3046463
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 393)
  AUTHORS   Siegel,D.L., Chang,T.Y., Russell,S.L. and Bunya,V.Y.
  TITLE     Isolation of cell surface-specific human monoclonal antibodies
            using phage display and magnetically-activated cell sorting:
            applications in immunohematology
  JOURNAL   J. Immunol. Methods 206 (1-2), 73-85 (1997)
   MEDLINE   97469098
   PUBMED    9328570
REFERENCE   2  (bases 1 to 393)
  AUTHORS   Chang,T.Y. and Siegel,D.L.
  TITLE     Genetic and immunological properties of phage-displayed human
            anti-Rh(D) antibodies: Implications for Rh(D) epitope topology
  JOURNAL   Blood 91 (8), 3066-3078 (1998)
   MEDLINE   98200617
   PUBMED    9516621
REFERENCE   3  (bases 1 to 393)
  AUTHORS   Chang,T.Y., Russell,S.L., Bunya,V.Y. and Siegel,D.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-JAN-1998) Path & Lab Med, University of Pennsylvania,
            36th & Hamilton, Philadelphia, PA 19104, USA
FEATURES             Location/Qualifiers
     source          1..393
                     /organism="synthetic construct"
                     /mol_type="mRNA"
                     /db_xref="taxon:32630"
                     /clone_lib="gamma 1 phage display library R03"
                     /focus
                     /clone="E03"
     CDS             <1..>393
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                     /codon_start=1
                     /transl_table=11
                     /product="anti-Rh(D) antibody VH segment"
                     /protein_id="AAC13447.1"
                     /db_xref="GI:3046464"
                     /translation="EVQLLESGVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQG
                     PGKGLEWVSSISNSNTYIYYADAVKGRFTISRDNAKNSLYLQMNSLRAEHTAVYCAR
                     DSRYSNFLRWVRSDGMDVWGQGTTVVSS"
     V_segment       1..>393
     misc_feature    1..18
                     /note="pComb3H"
     primer_bind     19..24
                     /note="VH1f/VH3f primer"
BASE COUNT       88 a     99 c    120 g    86 t
ORIGIN
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Query Match       100.0%;  Score 393;  DB 12;  Length 393;
Best Local Similarity   100.0%;
Matches 393;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTCAAGCCTGGGGGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTCAAGCCTGGGGGG 60

Qy   61 TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATAGCCATGCACTGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATAGCCATGCACTGG 120

Qy  121 GTCCGCCAGGGTCCAGGGAAGGGGCTGGAGTGGGTCTCATCCATTAGTAATAGTAATACT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GTCCGCCAGGGTCCAGGGAAGGGGCTGGAGTGGGTCTCATCCATTAGTAATAGTAATACT 180

Qy  181 TACATATACTACGCAGACGCAGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 TACATATACTACGCAGACGCAGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAG 240

Qy  241 AACTCACTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTACTACTGT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 AACTCACTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTACTACTGT 300

Qy  301 GCGAGAGATTCTAGATACTACAGTAATTTCCTCCGTTGGGTTCGGAGCGACGGTATGGACGTC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 GCGAGAGATTCTAGATACTACAGTAATTTCCTCCGTTGGGTTCGGAGCGACGGTATGGACGTC 360

Qy  361 TGGGGCCAAGGGACCACACGGTCATCGTCTCCTCA 393
          ||||||||||||||||||||||||||||||||||||
Db  361 TGGGGCCAAGGGACCACACGGTCATCGTCTCCTCA 393
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RESULT 3

LOCUS   AR160967   381 bp   DNA   linear   PAT 17-OCT-2001
DEFINITION   Sequence 96 from patent US 6255455.
ACCESSION   AR160967
VERSION   AR160967.1   GI:16226167
KEYWORDS   .
SOURCE   Unknown.
   ORGANISM   Unknown.
           Unclassified.
REFERENCE   1 (bases 1 to 381)
   AUTHORS   Siegel,D.L.
   TITLE   Rh(D)-binding proteins and magnetically activated cell sorting
           method for production thereof
   JOURNAL   Patent: US 6255455-A 96 03-JUL-2001;
FEATURES   Location/Qualifiers
      source   1..381
                        /organism="unknown"
BASE COUNT   87 a   98 c   113 g   83 t
ORIGIN

Query Match   92.58%;   Score 363.6;   DB 6;   Length 381;
Best Local Similarity   98.9%;   Pred. No. 2.2e-106;
Matches   366;   Conservative   0;   Mismatches   4;   Indels   0;   Gaps   0;

Qy   24 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
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Db   12 GCTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 71

Qy   84 CTCTGGATTCACCTTCAGTAGCTATAGCATGGCATGGGTCCGCCAGGGTCCAGGGAAGGG 143
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Db   72 CTCTGGATTCACCTTCAGTAGCTATAGCATGGCATGGGTCCGCCAGGGTCCAGGGAAGGG 131

Qy   144 GCTGGAGTGGGGTCTCATCCATTAGTAATAGTAATAGTTACATATACTACGGAAACAGTA 203
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Qy   204 GAAGGGCCGATTCACCATCTCCAGAGACAACACCCCAAGAACTCACTGTATCTGCAAATGAA 263
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Db   192 GAAGGGCCGATTCACCATCTCCAGAGACAACACCCCAAGAACTCACTGTATCTGCAAATGAA 251

Qy   264 CAGCCTGAGAGCCGAGGACACACGGCTGTGTACTACTGTGCGAGAGATTCTAGATACAGTAA 323
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Db   252 CAGCCTGAGAGCCGAGGACACACGGCTGTGTACTACTGTGCGAGAGATTCTAGATACAGTAA 311

Qy   324 TTTCCTCCGTTGGGGTTCGGGACGGATATGGACGTCTGGGGCCAAGGGACCACGGTCAT 383
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Db   312 TTTCCTCCGTTGGGGTTCGGGACGGATATGGACGTCTGGGGCCAAGGGACCACGGTCAT 371

Qy   384 CGTCTCCTCA 393
       ||||||||||
Db   372 CGTCTCCTCA 381

RESULT 4

LOCUS   AF044445   381 bp   mRNA   linear   SYN 31-OCT-2001
DEFINITION   Synthetic construct from Homo sapiens clone E01 anti-Rh(D) antibody
           VH segment mRNA, partial cds.
ACCESSION   AF044445
VERSION   AF044445.1   GI:3046461
KEYWORDS   .
SOURCE   synthetic construct
   ORGANISM   synthetic construct
           artificial sequences.
REFERENCE   1 (bases 1 to 381)
   AUTHORS   Siegel,D.L., Chang,T.Y., Russell,S.L. and Bunya,V.Y.
   TITLE   Isolation of cell surface-specific human monoclonal antibodies
           using phage display and magnetically-activated cell sorting:
           applications in immunohematology
   JOURNAL   J. Immunol. Methods 206 (1-2), 73-85 (1997)

MEDLINE   97469098
   PUBMED   9328570
REFERENCE   2 (bases 1 to 381)
   AUTHORS   Chang,T.Y. and Siegel,D.L.
   TITLE   Genetic and immunological properties of phage-displayed human
           anti-Rh(D) antibodies: implications for Rh(D) epitope topology
   JOURNAL   Blood 91 (8), 3066-3078 (1998)
   MEDLINE   98200617
   PUBMED   9531621
REFERENCE   3 (bases 1 to 381)
   AUTHORS   Chang,T.Y., Russell,S.L., Bunya,V.Y. and Siegel,D.L.
   TITLE   Direct Submission
   JOURNAL   Submitted (26-JAN-1998) Path & Lab Med, University of Pensylvania,
           36th & Hamilton, Philadelphia, PA 19104, USA
FEATURES   Location/Qualifiers
      source   1..381
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                        /db_xref="taxon:32630"
                        /clone_lib="gamma 1 phage display library R03"
                        /focus
      CDS   25..381
                        /organism="Homo sapiens"
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                        /db_xref="taxon:9606"
                        /clone="E01"
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                        /product="anti-Rh(D) antibody VH segment"
                        /protein_id="AAC13446.1"
                        /db_xref="GI:3046462"
                        /translation="EVQLLESGGGLVKPGGSLRLSCAASGFFSSYSMHWVRQAPGKG
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                        SNFLRWVRSDGMDVWGQGTTVIVSS"
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BASE COUNT   87 a   98 c   113 g   83 t
ORIGIN

Query Match   92.58%;   Score 363.6;   DB 12;   Length 381;
Best Local Similarity   98.9%;   Pred. No. 2.2e-106;
Matches   366;   Conservative   0;   Mismatches   4;   Indels   0;   Gaps   0;

Qy   24 GGTGGAGTCTGGGGGAGGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
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Db   12 GCTGGAGTCTGGGGGAGGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 71

Qy   84 CTCTGGATTCACCTTCAGTAGCTATAGCATGGCATGGGTCCGCCAGGGTCCAGGGAAGGG 143
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   72 CTCTGGATTCACCTTCAGTAGCTATAGCATGGCATGGGTCCGCCAGGGTCCAGGGAAGGG 131

Qy   144 GCTGGAGTGGGGTCTCATCCATTAGTAATAGTAATAGTTACATATACTACGGAAACAGTA 203
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Qy   204 GAAGGGCCGATTCACCATCTCCAGAGACAACACCCCAAGAACTCACTGTATCTGCAAATGAA 263
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Db   192 GAAGGGCCGATTCACCATCTCCAGAGACAACACCCCAAGAACTCACTGTATCTGCAAATGAA 251

Qy   264 CAGCCTGAGAGCCGAGGACACACGGCTGTGTACTACTGTGCGAGAGATTCTAGATACAGTAA 323
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Db   252 CAGCCTGAGAGCCGAGGACACACGGCTGTGTACTACTGTGCGAGAGATTCTAGATACAGTAA 311

Qy   324 TTTCCTCCGTTGGGGTTCGGGACGGATATGGACGTCTGGGGCCAAGGGACCACGGTCAT 383
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Db   312 TTTCCTCCGTTGGGGTTCGGGACGGATATGGACGTCTGGGGCCAAGGGACCACGGTCAT 371

Qy   384 CGTCTCCTCA 393
       ||||||||||
Db   372 CGTCTCCTCA 381

Left column:

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RESULT 5
LOCUS       HSA234196         435 bp    DNA    linear   PRI 10-DEC-1999
DEFINITION  Homo sapiens mRNA for Ig heavy chain variable region, clone
            C6/9/10.
ACCESSION   AJ234196
VERSION     AJ234196.1  GI:3821137
KEYWORDS    heavy chain; immunoglobulin superfamily; variable region.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 435)
AUTHORS     Noppe,S.M., Heirman,C., Bakkus,M.H., Brissinck,J., Schots,R. and
            Thielemans,K.
TITLE       The genetic variability of the VH genes in follicular lymphoma: the
            impact of the hypermutation mechanism
JOURNAL     Br. J. Haematol. 107 (3), 625-640 (1999)
MEDLINE     20050318
PUBMED      10583269
REFERENCE   2  (bases 1 to 435)
AUTHORS     Noppe,S.M.
TITLE       Direct Submission
JOURNAL     Submitted (23-OCT-1998) Noppe S.M., Laboratory of Physiology, Free
            University of Brussels Laarbeeklaan 103/E, 1090 Brussels, BELGIUM
FEATURES             Location/Qualifiers
     source          1..435
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /isolate="follicular lymphoma patient"
                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /clone="C6/9/10"
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BASE COUNT    93 a    104 c    135 g    103 t
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Query Match    77.9%;  Score 306;  DB 9;  Length 435;
Best Local Similarity    91.1%;
Matches 337;  Conservative 0;  Mismatches 30;  Indels 3;  Gaps 1;

Qy     24 GGTGGAGTGCTTGGGGAGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
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Db     69 GGTGGAGTGTTGGGGAGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 128

Qy     84 CTCTGGATTCACCTTCAGTAGCTATATAGCACTGGGTCCGCCCCAGGGTCCAGGGAAGGG 143
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Db    129 CTCTGGATTCACCTTCAGTAGCTATATAGCATGAAACTGGGTCCGCCCCAGGGTCCAGGGAAGGG 188

Qy    144 GCTGGAGTGGGTGTCTCATCCATTAGTAGTAATAGTAACTTACATATACTACGGAGACCCGAGT 203
          |||||||||||| ||||| |||||||||||||||||| |||||| ||| |||||||||||||
Db    189 GCTGGAGTGGGTGTCATCCATTAGTAGTAGTAGTTACAATATACCTACGGAGACTCAGT 248

Qy    204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCCAGAACTCACTGTATCTGCAAATGAA 263
          ||||||||||||||||| ||||||||| |||||| |||||||||||| ||||||||||||
Db    249 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCCAGAACTCACTGTATCTGCAAATGAA 308

Qy    264 CAGCCTGAGAGCCGCAGACACGGCTGTGTATTACTGTGCGAGAGATTCTAGATACAGTAA 323
          |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db    309 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATGAT---CAGTGG 365

Qy    324 TTTCCCTTCCGTTGTGGTTCGGACGCGACGGTATGGACGTGGGCCAAGGGGACCACGGTCAC 383
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Db    324 --------------------------------||-------------------------CGGTCAT 383
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Right column:

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RESULT 6
LOCUS       HSA519295         396 bp    mRNA    linear   PRI 14-JAN-2003
DEFINITION  Homo sapiens partial mRNA for IgM immunoglobulin heavy chain
            variable region (IGHV gene), clone ANBPM229.
ACCESSION   AJ519295
VERSION     AJ519295.1  GI:27753290
KEYWORDS    IGHV gene; immunoglobulin heavy chain; variable region.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 396)
AUTHORS     Lausen,B.F., Hougs,L., Schejbel,L., Heilmann,C. and Barington,T.
TITLE       Human memory B cells transferred by Allogeneic bone marrow
            transplantation contribute significantly to the antibody
            repertoire, but fail to re-enter the process of somatic mutation
            upon antigenic stimulation
JOURNAL     Unpublished
REFERENCE   2  (bases 1 to 396)
AUTHORS     Lausen,B.F., Hougs,L., Schejbel,L., Heilmann,C. and Barington,T.
TITLE       Direct Submission
JOURNAL     Submitted (22-NOV-2002) Paediatric Clinic II, section 4064, Juliane
            Marie Centre, University hospital Rigshospitalet, Blegdamsvej 9,
            Copenhagen DK-2100, Denmark
FEATURES             Location/Qualifiers
     source          1..396
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BASE COUNT    86 a    97 c    122 g    91 t
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Db    372 CGTCTCCTCA 381
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Qy    384 CGTCTCCTCA 393
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Db    366 CTGGTACCCCTCCTTAGCGTTAGCCGGGTATGGACGTCTGGGGGCCAAGGGACCACGGTCAC 425
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Qy    384 CGTCTCCTCA 393
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Db    366 CTGGTACCCCTCCTTAGCGTTAGCCGGGTATGGACGTCTGGGGGCCAAGGGACCACGGTCAC 425
Qy    384 CGTCTCCTCA 393
Db    426 CGTCTCCTCA 435
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RESULT 7

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LOCUS       AB066972      378 bp    mRNA    linear   PRI 02-JUL-2002
DEFINITION  Homo sapiens IGH mRNA for immunoglobulin heavy chain VHDJ region,
            partial cds, clone:aims0006h.
ACCESSION   AB066972
VERSION     AB066972.1  GI:21670000
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
            Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
            Miura,K. and Kurosawa,Y.
  TITLE     Construction and characterization of antibody libraries: isolation
            of therapeutic human antibodies and application to functional
            genomics
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 378)
  AUTHORS   Kurosawa,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JUL-2001) Yoshikazu Kurosawa, Institute for
            Comprehensive Medical Science, Fujita Health University,
            Immunology; Kutsukake-cho, Toyoake, Aichi 470-1192, Japan
            (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT     Please visit our web site
            URI:http://www.fujita-hu.ac.jp/1mmunity/.
FEATURES             Location/Qualifiers
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     gene            1..378
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Query Match             75.4%;  Score 296.2;  DB 9;  Length 396;
Best Local Similarity   89.0%;  Pred. No. 1.5e-84;
Matches  332;  Conservative   0;  Mismatches  38;  Indels  3;  Gaps  1;

Qy   24 GGTGGAGTCTGGGGGAGGCCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
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Db   24 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83

Qy   84 CTCTGGATTCACCTTCAGTAGCTATAGCACTCACGTGGGCTCCCTGGGGTCCAGGGAAGGG 143
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Db   84 CTCTGGATTCACCTTCAGTAGCTATAGCCATGAAGCTGGGTCCGCCAGGCTCCAGGGAAGGG 143

Qy  144 GCTGGAGTGGGTCTCANTCCATTAGTAGTAATAGTAACTTACATATACTACGCAGACCCAGT 203
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Db  144 GCTGGAGTGGGTCTCATNCCATTAGTAGTAGTTACATATACTACGCAGACTCAGT 203

Qy  204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
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Db  204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263

Qy  264 CAGCCTGAGAGCCGAGGACACGGCTGTGTACTACTGTGCGAGAGATTTAGATACAGTAA 323
         |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db  264 CAGCCTGAGAGCCGAGGACACGGCTGTATTACTGTGCTATTAGCATGAAACGAGACTCAGT 323

Qy  324 TTTC---CTCCGTTGGGTTCGGGGACGGGACGCGGTATGGACGTCTGGGGCCAAGGGACCACGGT 380
         |||  | |||||||||||||||||||||||||||||| ||  |||||||||||||||
Db  324 GTTCGGGGAGTTATATGTCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGT 383

Qy  381 CATCGTCTCCTCA 393
         |||||||||||||
Db  384 CACCGTCTCCTCA 396
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RESULT 8

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LOCUS       AF062202      435 bp    mRNA    linear   PRI 08-MAY-2001
DEFINITION  Homo sapiens clone 48u-42 immunoglobulin heavy chain variable
            region (IGH) mRNA, partial cds.
ACCESSION   AF062202
VERSION     AF062202.1  GI:3170866
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 435)
  AUTHORS   Wang,X. and Stollar,B.D.
  TITLE     Immunoglobulin VH gene expression in human aging
  JOURNAL   Clin. Immunol. 93 (2), 132-142 (1999)
   MEDLINE   99459182
   PUBMED    10527689
REFERENCE   2  (bases 1 to 435)
  AUTHORS   Wang,X. and Stollar,B.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-APR-1998) Biochemistry Department, Tufts University
            School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA
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     source          1..435
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BASE COUNT   88 a   89 c  123 g   78 t
ORIGIN

Query Match             74.8%;  Score 294;  DB 9;  Length 378;
Best Local Similarity   89.6%;  Pred. No. 7.9e-84;
Matches  328;  Conservative   0;  Mismatches  35;  Indels  3;  Gaps  1;

Qy   24 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
Db   12 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 71

Qy   84 CTCTGGATTCACCTTCAGTAGCTATAGCATGAACTGGGTCCGCCAGGCTCCAGGGAAGGG 143
Db   72 CTCTGGATTCACCTTCAGTAGCTATAGCATGAACTGGGTCCGCCAGGCTCCAGGGAAGGG 131

Qy  144 GCTGGAGTGGGTCTCATNAATAGTAATAGTAACATACATATACTACGCAGACGCAGT 203
Db  132 GCTGGAGTGGGTCTCATCCATTAGTAGTAGTAGTATACATATACTACGCAGACTCAGT 191

Qy  204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
Db  192 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 251

Qy  264 CAGCCTGAGAGCCGAGGACACGGCTGTGTACTACTGTGCGAGAGATTCTAGATACAGTAA 323
Db  252 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGAAGTAGTGGT 311

Qy  324 TTTCCTCCGTTGGGTTCGGGGACGGGACGCGGTATGGACGTCTGGGGCCAAGGGACCACGGTCAT 383
Db  312 TCGGGGCAAATAAGG---GCTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCAC 368

Qy  384 CGTCTC 389
Db  369 CGTCTC 374
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Query Match  74.7%;  Score 293.6;  DB 9;  Length 435;
Best Local Similarity  89.2%;          Pred. No. 1.1e-83;
Matches 330;  Conservative 0;  Mismatches 34;  Indels 6;  Gaps 1;

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Db   69 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC  128

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Qy  144 GCTGGAGTGGGGTCTCATCCATTAGTAATAGTAATACTTACATATATTACGACGCCAGT  203
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Qy  204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA  263
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Db  249 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA  308

Qy  264 CAGCCTGAGAGCCGAGGACACGGCTGTGTACTACTGTGCGAGAGATTCTAGATACAGTAA  323
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Db  309 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATGTCGAGGAGGCTAC  368

Qy  324 TTTCCTCCGTTCGGGTTCGGAGGCGACGGTGTATGGACGTCTGGGGCCAAGGGACCGTCAT  383
                                  |||  ||||||||||||||||||||||||||||||| |||
Db  369 GGTGACTTACGT------ACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCAC  422

Qy  384 CGTCTCCCTCA  393
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Db  423 CGTCTCCCTCA  432
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RESULT 9

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FEATURES             Location/Qualifiers
     source          1. .402
                         /organism="Homo sapiens"
                         /mol_type="mRNA"
                         /db_xref="taxon:9606"
                         /cell_type="B-lymphocyte"
                         /rearranged
                         /note="sample GN28"
     gene            <1. >402
                         /gene="IGVH"
     CDS             <1. >402
                         /gene="IGVH"
                         /function="immune response"
                         /codon_start=1
                         /product="immunoglobulin heavy chain variable region"
                         /translation="EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKG
                         LEWVSSISSSSSYIYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGGLL
                         WFGELLSYYYYGMDVWGQGTTVTVSSGSASA"
                         /db_xref="GI:5679518"
                         /protein_id="CAB51733.1"
BASE COUNT    89 a    100 c    125 g    88 t
ORIGIN

Query Match  74.68%;  Score 293.2;  DB 9;  Length 402;
Best Local Similarity  88.3%;          Pred. No. 1.5e-83;
Matches 332;  Conservative 0;  Mismatches 38;  Indels 6;  Gaps 1;

Qy   24 GGTGGAGTCTGGGGGAGGCGTTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC   83
         |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   12 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC   71

Qy   84 CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG  143
         ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   72 CTCTGGATTCACCTTCAGTAGCTATAGCATGAACTGGGTCCGCCAGGCTCCAGGGAAGGG  131

Qy  144 GCTGGAGTGGGGTCTCATCCATTAGTAATAGTAATACTTACATATATTACGACGCCAGT  203
         ||||||||||||||||||||||||||||| || | |    |||||||||| ||||||||
Db  132 GCTGGAGTGGGGTCTCATCCATTAGTAGTAGTAGTTACATATATTACTACGACGCCAGT  191

Qy  204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA  263
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  192 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA  251

Qy  264 CAGCCTGAGAGCCGAGGACACGGCTGTGTACTACTGTGCGAGAG-----ATTCTAGATA  317
         ||||||||||||||||||||||||||||||| ||||||||||||     ||||||||||
Db  252 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG-----ATTCTAGATA  311

Qy  318 CAGTAATTTCCTCCGTTGGGGTTCGGACGCGACACGGCGTATGGACGTCTGGGGCCAAGGGACCAC  377
         |   || | |||||                    |||||||||||||||||||||||||||||||
Db  312 CGGGGAGTTATTATCCTACTACTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCAC  371

Qy  378 GGTCATCGTCTCCTCA  393
         ||||| ||||||||||
Db  372 GGTCACCGTCTCCTCA  387
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RESULT 10

REFERENCE   1 (bases 1 to 378)
AUTHORS   Lausen,B.F., Hougs,L., Schejbel,L., Heilmann,C. and Barington,T.
TITLE   Human memory B cells transferred by Allogeneic bone marrow
             transplantation contribute significantly to the antibody
             repertoire, but fail to re-enter the process of somatic mutation
             upon antigenic stimulation
             Unpublished
REFERENCE   2 (bases 1 to 378)
AUTHORS   Lausen,B.F., Hougs,L., Schejbel,L., Heilmann,C. and Barington,T.
TITLE   Direct Submission
JOURNAL   Submitted (22-NOV-2002) Paediatric Clinic II, section 4064, Juliane
             Marie Centre, University hospital Rigshospitalet, Blegdamsvej 9,
             Copenhagen DK-2100, Denmark
FEATURES   Location/Qualifiers
     source   1..378
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="ANBPM223"
     gene   1..378
                     /gene="IGHV"
                     /rearranged
     CDS   <1..>378
                     /gene="IGHV"
                     /codon_start=1
                     /product="immunoglobulin heavy chain variable region"
                     /protein_id="CAD60353.1"
                     /db_xref="GI:27753285"
                     /translation="EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKG
                     LEWVSISSSSSYIYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCASIGGI
                     TGDNYYYYGMDVWGQGTTVTVSS"
     V_region   <1..>378
                     /gene="IGHV"
     V_segment   1..294
                     /gene="IGHV"
                     /note="germline gene: VH3-21"
     N_region   295..304
                     /gene="IGHV"
     D_segment   305..314
                     /gene="IGHV"
                     /note="germline gene: D7-27"
     N_region   315..318
                     /gene="IGHV"
     J_segment   319..378
                     /gene="IGHV"
                     /note="germline gene: JH6b1"
BASE COUNT   88 a   94 c   116 g   80 t
ORIGIN

Query Match   74.2%;   Score 291.6;   DB 9;   Length 378;
Best Local Similarity 88.6%;
Matches 328;   Conservative 0;   Mismatches 39;   Indels 3;   Gaps 1;

Qy   24 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
          ||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db   12 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 71

Qy   84 CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGGTCCAGGGAAGG 143
          |||||||||||||||||||| ||||||||||| |||||||||||||||||||||||||||
Db   72 CTCTGGATTCACCTTCAGTAGCTATAGCATGAACTGGGTCCGCCAGGCTCCAGGGAAGGG 131

Qy   144 GCTGGAGTGGGTGTCTCATCCATTAGTAATAGTAAATACTTACATATATACGCAGACGCAGT 203
          |||||||||||| ||||||||||||||||||||||| |||||||||||||||||||||
Db   132 GCTGGAGTGGGTCTCATCCATTAGTAGTAGTAGTAGTAGTACATATATACCAGGACTCAGT 191

Qy   204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   192 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 251

Qy   264 CAGCCTGAGAGCCGAGCACACGGCTGTGTACTACTGTGCGAGAGATTCTTAGATACAGTAA 323
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   264 CAGCCTGAGGGCCGAGGACACGGGCTGTGTATTACTGTGCGAGAGATTGGGGGGA---ATAAC 308

Db   252 CAGCCTGAGGGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGCATTGGGGGGA---ATAAC 308
          |||||||| |||||||||||||||||||||||||||||||
Db   309 TGGGGACAACTACTACTACTACTACTACGGTATGGACGTCTGGGGGCCAAGGGACCACGGTCAC 368

Qy   384 CGTCTCCTCA 393
          |||||||||
Db   369 CGTCTCCTCA 378

RESULT 11
LOCUS   HSU77374   384 bp   mRNA   linear   PRI 14-MAY-2001
DEFINITION Homo sapiens clone IRM-3HC IgM heavy chain variable region mRNA,
            partial cds.
ACCESSION   U77374
VERSION   U77374.1 GI:1679767
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 384)
  AUTHORS   Aguilera,I., Melero,J., Nunez-Roldan,A. and Sanchez,B.
  TITLE   Molecular structure of eight human autoreactive monoclonal
            antibodies
  JOURNAL   Immunology 102 (3), 273-280 (2001)
  MEDLINE   21195372
   PUBMED   11298825
REFERENCE   2 (bases 1 to 384)
  AUTHORS   Aguilera,I.
  TITLE   Direct Submission
  JOURNAL   Submitted (05-NOV-1996) Immunology, Hospital U. Virgen Del Rocio,
            Manuel Siurot, s/n., Seville, 41013, Spain
FEATURES   Location/Qualifiers
     source   1..384
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IRM-3HC"
     CDS   <1..>384
                     /codon_start=1
                     /product="IgM heavy chain variable region"
                     /protein_id="AAB19221.1"
                     /db_xref="GI:1679768"
                     /translation="EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKG
                     LEWVSYISSSSSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDNYY
                     DSSGSLRRYYYGMDVWGQGTTVTVSS"
BASE COUNT   91 a   90 c   116 g   87 t
ORIGIN

Query Match   73.3%;   Score 288.2;   DB 9;   Length 384;
Best Local Similarity 87.8%;
Matches 327;   Conservative 0;   Mismatches 43;   Indels 3;   Gaps 1;

Qy   24 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
          |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   12 GGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 71

Qy   84 CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGGTCCAGGGAAGG 143
          ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   72 CTCTGGATTCACCTTCAGTAGCTATAGCATGAGCATGGGTCCGCCAGGCTCCAGGGAAGGG 131

Qy   144 GCTGGAGTGGGTGTCTCATCCATTAGTAATAGTAAATACTTACATATATACGCAGACGCAGT 203
          ||||||||||||||||||||||||||||||| ||||||||||||||||| |||||||||||
Db   132 GCTGGAGTGGGTGTTTCATCCATTAGTAGTAGTAGTAGTACCATATATACCAAGGACTCTGT 191

Qy   204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
          |||||||||||||||||||||||||| ||||||||| |||||||||||||||||||||||
Db   192 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 251

Qy   264 CAGCCTGAGAGCCGAGCACACGGCTGTGTACTACTGTGCGAGAG---ATTCTTAGATACAG 320
          |||||||| ||||||||||||||||||||||||||||||||||| || ||||||||||
Db   264 CAGCCTGAGGGCCGAGGACACGGGCTGTGTACTACTGTGCGAGAG---ATTCTAGATACAG 320

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Qy    252 CAGGCTGAGAGCCGGGAGACAGCGGATCGTGTATTACTGTGCGAGAGACAATTACTATGATAG 311
          ||||||||||||||||||||||||||||||||||||||||||||  |||  |||
Db    252 CAGGCTGAGAGCCGGGAGACAGCGGATCGTGTATTACTGTGCGAGAGA             311

Qy    321 TAATTTCCTCCGTTGGGTTCGGGACGACGTCTGGGGCCAAGGGACCACGGT 380
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    321 TAGTGGTTGTCCCTGAGGAGGATACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGT 380

Qy    312 TAGTGGTTGTCCCTGAGGAGGATACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGAGT 131
          |||||||||||||||||||||||||||||||||||||||||||||||||||  |
Db                                                              393

Qy    381 CATCGTCTCCCTCA 393
          |||||||||||||
Db    381 CATCGTCTCCCTCA 191

Qy    372 CACCGTCTCCCTCA 384
          |||||||||||||
Db    372 CACCGTCTCCCTCA 384
```

RESULT 12

```
LOCUS       HUMVH3H               385 bp    mRNA    linear    PRI 27-MAR-2002
DEFINITION  Human mRNA for immunoglobulin M (IgM), partial cds (VH3-N-D-N-JH6),
            clone H2-47E.
ACCESSION   D83682
VERSION     D83682.1    GI:1213571
KEYWORDS    IgM; immunoglobulin M.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hakoda,M., Kamatani,N., Hayashimoto-Kurumada,S., Silverman,G.J.,
            Yamanaka,H., Terai,C. and Kashiwazaki,S.
  TITLE     Differential binding avidities of human IgM for staphylococcal
            protein A derive from specific germ-line VH3 gene usage
  JOURNAL   J. Immunol. 157 (7), 2976-2981 (1996)
  PUBMED    8816405
REFERENCE   2  (bases 1 to 385)
  AUTHORS   Hakoda,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-FEB-1996) Masayuki Hakoda, Tokyo Women's Medical
            College, Institute of Rheumatology; 10-22 Kawada-cho, Shinjuku-ku,
            Tokyo 162, Japan (Tel:3-5269-1725, Fax:3-5269-1726)
FEATURES             Location/Qualifiers
     source          1..385
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="H2-47E"
                     /cell_type="B-cell"
                     /tissue_type="Blood"
     CDS             <1..>385
                     /rearranged
                     /note="VH3-N-D-N-JH6"
                     /codon_start=1
                     /product="IgM"
                     /protein_id="BAA12049.1"
                     /db_xref="GI:1871483"
                     /db_xref="IMGT/LIGM:D83682"
                     /translation="EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMNWIRQAPGKG
                     LEWVSYISSSSSTIIYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARALTY
                     YDSSGYGYYGMDVWGQGTTVTVSS"
     V_segment       1..294
                     /note="VH3 gene"
     N_region        295..329
                     /note="N-D-N region"
     J_segment       330..385
                     /note="JH6 gene"
ORIGIN
BASE COUNT      89 a     92 c    115 g     89 t
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Query Match        72.9%;  Score 286.6;  DB 9;  Length 385;
Best Local Similarity   87.4%;  Pred. No. 2e-81;
Matches  326;  Conservative   0;  Mismatches   44;  Indels   3;  Gaps   1;

Qy    24 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    24 GGTGGAGTCTGGGGGAGGCTTGGTGACAGCCTGGGGGTCCCTGAGACTCTCCTGTGCAGC 71
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Qy    84  CTCTGGATTCACCTTCAGTAGCTATAGCATGAACTGGGTCCGGGCCAGGGGAAGG 143
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    72  CTCTGGATTCACCTTCAGTAGCTATAGCATGAACTGGGTCCGGGCCAGGGGAAGG 131

Qy    144 GCTGGAGTGGGTCTCATCCATTAGTAGTAGTGGTAATATACATACACAGACGCAGT 203
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    132 GCTGGAGTGGGTTTCATACATAGTAGTAGTAGTAGTACCATATACTACGCAGACTCTGT 191

Qy    204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAAAATGAA 263
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db    192 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAAAATGAA 251

Qy    264 CAGCCTGAGAGCCGAGCACACGGCTGTGTATTACTACTGTGCGAGAGAT---TCTAGATACAG 320
          |||||||||||||||||||||||||||||||||||||||||||||||||||   |
Db    252 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGAGCTCACGTATTACTA 311

Qy    321 TAATTTCCTCCGTTGGGTTCGGGACGACGTCTGGGGCCAAGGGACCACGGT 380
          |||||||||||||||||||||||||||||||||||
Db    312 TGATAGTAGTGGTTATGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGT 371

Qy    381 CATCGTCTCCCTCA 393
          |||||||||||||
Db    372 CACCGTCTCCCTCA 384
```

RESULT 13

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LOCUS       AF032350              438 bp    mRNA    linear    PRI 12-DEC-2001
DEFINITION  Homo sapiens variable immunoglobulin anti-HLA heavy chain (IgH)
            mRNA, partial cds.
ACCESSION   AF032350
VERSION     AF032350.1    GI:2654033
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 438)
  AUTHORS   Loeffler,D., Welschof,M., Goldmann,S.F. and Wolpl,A.
  TITLE     Recognition of HLA-DR1/DRB1*0101 molecules presenting HLA-A2
            derived peptides by a human recombinant antibody, Fab-5 A1
  JOURNAL   Eur. J. Immunogenet. 25 (5), 339-347 (1998)
  PUBMED    9805656
REFERENCE   2  (bases 1 to 438)
  AUTHORS   Loeffler,D., Woelpl,A. and Goldmann,S.F.
  TITLE     Immunoglobulin variable gene analysis of human HLA alloantibodies
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 438)
  AUTHORS   Loeffler,D., Woelpl,A. and Goldmann,S.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-NOV-1997) Department of Transplantation Immunology,
            Red Cross Blood Bank Ulm, Helmholtzstr. 10, Ulm 89081, Germany
FEATURES             Location/Qualifiers
     source          1..438
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /map="14q32"
                     /cell_line="EBV transformed human B-cell line fused to
                     heteromyeloma"
     gene            <1..>438
                     /gene="IgH"
     CDS             <1..>438
                     /gene="IgH"
                     /codon_start=1
                     /product="variable immunoglobulin anti-HLA heavy chain"
                     /protein_id="AAB87970.1"
                     /db_xref="GI:2654034"
                     /translation="GGGLFKPGGSLRLSCAASGFTFRSHGMNVWVRQAPGKGLEWVSSI
                     SSSTSYIYANSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDRPGGYCSGSVS
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BASE COUNT
ORIGIN

Query Match "CYSTYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAA"
          93 a 127 c 128 g   90 t

Query Match   72.5%;   Score 284.8; DB 9; Length 438;
Best Local Similarity 88.3%; Pred. No. 7.7e-81;
Matches 323; Conservative 0; Mismatches 37; Indels 6; Gaps 1;

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Qy   34 GGGGGAGGCCTGGTCTCAAGCCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTC  93
        |||||||||||||| ||||| ||||||||||||||||||||||||| |||||||||||||||
Db    1 GGGGGAGGCCTGGTTCAAGCCTGGGGGGGTCCCTGAGACTCTCGTGTGCAGCCTCTGGATTC  60

Qy   94 ACCTTCAGTAGCTATAGCATGCACTGGGTGGTCCGCCAGGCTCCAGGGAAGGGCTGGAGTGG 153
        ||||||| ||| |||| ||| ||| ||||||||||||||||||||||||||||||||||||
Db   61 ACCTTCAGGAGCCACGGCCATGAACTGGGTGGTCCGCCAGGCTCCAGGGAAGGGCTGGAGTGG 120

Qy  154 GTCTCATCCATTAGTAATAGTAATAATACTTACATAATACGCACGCACGCAGTGAACGGCCGA 213
        |||||||||||||| || || |||| ||||||| |||||| ||||||||| ||||| |||||||
Db  121 GTCTCATCCATTAGTAGTAGTAGTTACATATACTCACGCAAACTCAGTGAAGGGCCGA 180

Qy  214 TTCACCATCTCCAGAGACAAGCCCAAGAACTCACTGTATCTGCAAATGAACAGCCTGAGA 273
        |||||||||||||||||||| || |||||||||||||| ||||||||||||||||||||
Db  181 TTCACCATCTCCAGAGACAACGCCAAGAAACTCACTGTAICTGCAAATGAACAGCCTGAGA 240

Qy  274 GCCGAGCACACGGCCGTGTGTACTACTGTGCGAGAGAT------TCTAGATACAGTAATTTC 327
        |||||| |||||||||||| || |||||| |||||||        ||| ||| ||||| |||
Db  241 GCCGAGGACACGGCCGTGTATTACTGTGCCGAGAGATCGGCCGCGGGGGGATATTGTAGTGGGC 300

Qy  328 CTCCGTTGGGTTCGGAGCGCACGGTATGGACGTCTCGGGGGGACCACGGTCATCGTC 387
           |||    |  |||  |||||||||||||||||  ||||| |||||||||| ||||
Db  301 GTTAGTTGTTTACTCTACGTATGGACGTCTGGGGGCCAAGGGACCACGGTCACCGTC 360

Qy  388 TCCTCA 393
        ||||||
Db  361 TCCTCA 366
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RESULT 14
LOCUS   AF170095   372 bp   DNA   linear   PRI 02-MAY-2001
DEFINITION Homo sapiens isolate MCL-BV/128 immunoglobulin heavy chain VDJ
            region (IGHθ) gene, IGHθ-F allele, partial cds.
ACCESSION   AF170095
VERSION   AF170095.1 GI:5917697
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 372)
  AUTHORS   Laszlo,T., Nagy,M., Kelenyi,G. and Matolcsy,A.
  TITLE   Immunoglobulin V(H) gene mutational analysis suggests that blastic
            variant of mantle cell lymphoma derives from different stages of
            B-cell maturation
  JOURNAL   Leuk. Res. 24 (1), 27-31 (2000)
  MEDLINE   20098130
   PUBMED   10634642
REFERENCE   2 (bases 1 to 372)
  AUTHORS   Matolcsy,A.
  TITLE   Direct Submission
  JOURNAL   Submitted (21-JUL-1999) Department of Pathology, University Medical
            School of Pecs, Szigeti ut 12, Pecs, Baranya 7624, Hungary
FEATURES   Location/Qualifiers
     source   1..372
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /isolate="MCL-BV/128"
                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /map="14q32"
                     /cell_type="B-cell"
                     /tissue_type="mantle cell blastic variant of non-Hodgkin's
                     lymphoma"
     gene   <1..>372
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                     /allele="F"
     mRNA   <1..>372
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                     /product="immunoglobulin heavy chain VDJ region"
     CDS   <1..>372
                     /gene="IGHθ"
                     /codon_start=1
                     /product="immunoglobulin heavy chain VDJ region"
                     /protein_id="AAD55996.1"
                     /db_xref="GI:5917698"
                     /translation="VQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGL
                     EWVSSISSSSYIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDIYSS
                     SWDAYYYYMDVWGKGNPGTVSS"

BASE COUNT
ORIGIN

Query Match
          89 a   93 c 111 g   79 t

Query Match   72.3%;   Score 284; DB 9; Length 372;
Best Local Similarity 87.6%; Pred. No. 1.4e-80;
Matches 324; Conservative 0; Mismatches 40; Indels 6; Gaps 1;

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Qy   24 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGC  83
        ||||||||||||||||||| |||||||||||||||||||||||||||||||| |||||||
Db    9 GGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGGGGGGTCCCTGAGACTCTCGTGTGCAGC  68

Qy   84 CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG 143
        |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   69 CTCTGGATTCACCTTCAGTAGCTATAGCATGAACTGGGTCCGCCAGGCTCCAGGGAAGGG 128

Qy  144 GCTGGAGTGGGGTCTCATCCATTCATTAGTAATAGTAATAACTTACACGATATACTACGGCAGAGGCCGAGT 203
        ||||||||||||||||||||||  ||||| || || || |||||| || |||||||||||| |||  |||
Db  129 GCTGGAGTGGGGTCTCATCCATTAGTAGTAGTAGTTACATATACTACGGCAGAGACTCAGT 188

Qy  204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  189 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 248

Qy  264 CAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGATTCTAGATACAGTAA 323
        ||||||||||||||||||||||||||||||||||||||||||| |||
Db  249 CAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGC--- 305

Qy  324 TTTCCTCCGTTGGGTTCGGAGCGCACGGTATGGACGTCTGGGGGGCCAAGGGACCACGGTCAT 383
           ||  |       | | | |||  ||||||||||||||||||||| ||||||||||
Db  306 ---CACCTGGGACGCAPACTACTACTACATGGACGTCTGGGGCGCCAAAGGGACCACCCTGGTAC 362

Qy  384 CGTCTCCTCA 393
        ||||||||||
Db  363 CGTCTCCTCA 372
```

RESULT 15
LOCUS   HSA555251   387 bp   mRNA   linear   PRI 15-APR-2003
DEFINITION Homo sapiens partial mRNA for immunoglobulin heavy chain variable
            region (IGHV gene), isolate B-CLL.G002.
ACCESSION   AJ555251
VERSION   AJ555251.1 GI:29892968
KEYWORDS   IGHV gene; immunoglobulin heavy chain; variable region.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Fais,F., Morabito,F., Stelitano,C., Callea,V., Zanardi,S.,
            Scudelletti,M., Varese,P., Ciccone,E. and Grossi,C.
  TITLE   CD1d on B-chronic lymphocytic leukemia cells mediates
            a-galactosylceramide presentation to natural killer T lymphocytes
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 387)
  AUTHORS   Fais,F.
  TITLE   Direct Submission

RESULT 16

```
LOCUS       AF174081              375 bp    mRNA    linear   PRI 08-MAY-2001
DEFINITION  Homo sapiens clone sc48u-100 immunoglobulin heavy chain variable
            region (IgH) mRNA, partial cds.
ACCESSION   AF174081
VERSION     AF174081.1  GI:5834121
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 375)
  AUTHORS   Wang,X. and Stollar,B.D.
  TITLE     Immunoglobulin VH gene expression in human aging
  JOURNAL   Submitted (03-APR-2003) Fais F., Department of Experimental
            medicine, Human Anatomy Section, Via De Toni 14, 16132, Genova,
            ITALY
FEATURES             Location/Qualifiers
     source          1..387
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /isolate="B-CLL G002"
                     /db_xref="taxon:9606"
                     /cell_type="chronic lymphocyte leukemia B-cell"
     gene            1..387
                     /rearranged
                     /gene="IGHV"
     CDS             <1..>387
                     /gene="IGHV"
                     /codon_start=1
                     /product="immunoglobulin heavy chain variable region"
                     /protein_id="CAD87736.1"
                     /db_xref="GI:29829969"
                     /translation="EVQLVESGGGLVKPGGSLRLSCAASGFFPSSYSMNWVRQAPGKG
                     LEWVSSISSSSTIYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARASNI
                     VVPAAIYGWDYFDYWGQGTLVTVSSG"
BASE COUNT       87 a      116 g      98 c      86 t
ORIGIN
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Query Match        72.0%;  Score 283;  DB 9;  Length 387;
Best Local Similarity  88.5%;  Pred. No. 2.9e-80;
Matches 330;  Conservative  0;  Mismatches 40;  Indels  3;  Gaps  2;

Qy          24 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
               |||||||||||||||||||||||||||||||||| ||||||| |||||||||||||||||
Db          12 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 71

Qy          84 CTCTGGATTCACCTTCAGTAGCTATTAGCACTGGGTTCCGCCAGGGGTCCAGGGAAGGG 143
               |||||||||||||||||||| || ||||||||||||||||||| |||||||||||||||
Db          72 CTCTGGATTCACCTTCAGTAGCTATTAGCATTAGCATGAACTGGGTTCCGCCAGGCTCCAGGGAAGGG 131

Qy         144 GCTCGGAGTGGGTCTCATCCATTAGTAATAGTAATAGTTACATATAACTACGGAGACGCAGT 203
               ||||||||||||||||||||||||| || || || ||||||||| ||||||||||||||||
Db         132 GCTCGGAGTGGGTCTCATCCATTAGTAGTAGTTACATATAACTACGGAGACTCAGT 191

Qy         204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
               ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db         192 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 251

Qy         264 CAGCCTGAGAGCCGAGGACACGGCTGTGTGTATTACTACTGTGCGAGAGATTCTA--GATACAGT 321
               |||||||||||||||||||||||| |||||||| |||||||||||||||||||  ||||||||
Db         252 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTACTGTGCGAGAGACTCTGT 311

Qy         322 AATTTCCTCCCGTTGGGTTCGG--AGGACGGTATGGGACGTCTGTGGGGCCAAGGGACCACGGT 380
               ||||||| ||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db         312 AGTACGACGTCTGCTAACTACGGCTGGGACTACTTTGACTACTGGGGCCAGGGAACCCTGGT 371

Qy         381 CATGTCGTCTCCCTCA 393
               |||||||||||||||
Db         372 CACCGTCTCCTCA 384
```

RESULT 17

```
LOCUS       HSY12442              389 bp    DNA     linear   PRI 15-JAN-1998
DEFINITION  H.sapiens IgH gene, partial isolate lymphoma 222.
ACCESSION   Y12442
VERSION     Y12442.1  GI:2073423
KEYWORDS    CDR3 region; constant region; heavy chain; immunoglobulin.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
REFERENCE   2  (bases 1 to 375)
  AUTHORS   Wang,X. and Stollar,B.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-1999) Biochemistry Department, Tufts University
            School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA
FEATURES             Location/Qualifiers
     source          1..375
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="sc48u-100"
                     /cell_type="peripheral blood B lymphocyte"
                     /note="single cell RT-PCR from elderly repertoire 48u"
     gene            <1..>375
                     /gene="IgH"
     CDS             <1..>375
                     /gene="IgH"
                     /codon_start=1
                     /product="immunoglobulin heavy chain variable region"
                     /protein_id="AAD58027.1"
                     /db_xref="GI:5834122"
                     /translation="EVQLVESGGGLVQPGGSLRLSCAASGFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDWSS
                     LEWVSYISSSSTIYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDWSS
                     SQYYYYGMDVWGQGTTLTVSSG"
BASE COUNT       85 a      117 g      90 c      83 t
ORIGIN
```

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Query Match        71.1%;  Score 279.6;  DB 9;  Length 375;
Best Local Similarity  87.0%;  Pred. No. 3.7e-79;
Matches 322;  Conservative  0;  Mismatches 39;  Indels  9;  Gaps  1;

Qy          24 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          12 GGTGGAGTCTGGGGGAGGCTTGGTGCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 71

Qy          84 CTCTGGATTCACCTTCAGTAGCTATAGCATAGCATTAGCAGCCTGGGGGGTCCCTGAGAACTGGGTTCCGCCAGC 143
               ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db          72 CTCTGGATTCACCTTCAGTAGCTATAGCATGAACTGGGTTCGCCAGGCTCCAGGGAAGGG 131

Qy         144 GCTGGAGTGGGTCTCATCCATTAGTAAATAGTAATAAATACTTACATTACATTATATACTACGCAGACGCAGT 203
               ||||||||||||||||||||||| | |||||||||| || ||||||||||||||||||||
Db         132 GCTGGAGTGGGTTTCATACATTAGTAGTAGTAGTACCATATACTACGCAGACTCTGT 191

Qy         204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         192 GAAGGGCCGATTCACCATCTCCAGAGACAACTCCAAGAACTCACTGTATCTGCAAATGAA 251

Qy         264 CAGCCTGAGAGCCGCAGCACACGCCGCTGTGTACTACTGTGCGAGAGAGAGATTCTAGATACAGTAA 323
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         252 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTACTGTGCGAGAGAGAATTGGAGCTCGTCGCA 311

Qy         324 TTTCCTCCCGTTGGGGTTCCGACGCGACGGTATGGGACGTCTGGGGCCCAAGGGACCACGGTGCAT 383
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         312 GTACTACTACT--------ACTACGGTATGGACGTCTGGGGCCAAGGGACCACGCTCAC 362

Qy         384 CGTCTCCCTCA 393
               |||  |||||
Db         363 CGTCTCGTCA 372
```

ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS   van Belzen,N., Hupkes,P.E., Doekharan,D., Hoogeveen-Westerveld,M.,
            Dorssers,L.C. and van't Veer,M.B.
TITLE   Detection of minimal disease using rearranged immunoglobulin heavy
            chain genes from intermediate- and high-grade malignant B cell
            non-Hodgkins lymphoma
JOURNAL   Leukemia 11 (10), 1742-1752 (1997)
MEDLINE   97464475
PUBMED   9324296
REFERENCE   2 (bases 1 to 389)
AUTHORS   Van Belzen,N.
TITLE   Direct Submission
JOURNAL   Submitted (05-APR-1997) N. Van Belzen, Erasmus University
            Rotterdam, Department of Hematology, PO Box 1738, 3000 DR
            Rotterdam, NETHERLANDS
FEATURES   Location/Qualifiers
     source   1..389
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /isolate="lymphoma 222"
                     /db_xref="taxon:9606"
                     /tissue_type="lymphoma"
                     /dev_stage="adult"
                     /rearranged
     CDS   <1..>389
                     /codon_start=3
                     /product="immunoglobulin heavy chain"
                     /protein_id="CAA73050.1"
                     /db_xref="GI:2073424"
                     /translation="VQLVESGGGLVKPGGSLRLSCAASGFTFSSHSMSNWVRQAPGKGL
                     EWVSISSSSSYIYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREPVEM
                     PTIFRNIQSGDAFDIWGQGTMVTVSSG"
     C_region   296..339
                     /product="Constant region of Ig heavy chain"
                     /note="CDR3 domain"
BASE COUNT   94 a   93 c   116 g   86 t
ORIGIN
Query Match   70.9%; Score 278.8; DB 9; Length 389;
Best Local Similarity   85.9%; Pred. No. 6.7e-79;
Matches 323; Conservative 0; Mismatches 47; Indels 6; Gaps 1;

Qy   24 GGTGGAGTCTGGGGGAGGCGTTGGTCAACCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC   83
           |||| ||||| |||||||||| |||| ||||||||||| ||||||||||||||||||
Db   11 GGTGGAGTCGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC   70

Qy   84 CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG 143
           |||||||||||||||||||||||||||||||||| |||||||||| ||||||||||||||
Db   71 CTCTGGATTCACCTTCACTAGTCATAGCATGAACTGGGTCCGCCAGGCTCCAGGGAAGGG 130

Qy   144 GCTGGAGTGGGTCTCATCCATTAGTAATAGTAATACTTACCATACGGCAGCAGACGCAGT 203
           || || ||||| ||||||||||||||||| |||||||| ||| |||||||||||||||||
Db   131 GCTGGAGTGGGTGTCATCCATTAGTAGTAGTTACATATTACACGGCAGCAGACTCAGT 190

Qy   204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
           |||||||||||||||||||||||| |||||||||||||||||||||||||||| ||||||
Db   191 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 250

Qy   264 CAGCCTGAGAGCCGAGCACACGCGCTGTGTACTACTGTGCGAGAGATTCTTAGATA----- 317
           ||||||||||||||||||||| |||||||||||||||||||||||||||| |||||
Db   251 CAGCCTGAGAGCCGAGCACACGCGCTGTATTACTGTGCGAGAGAAACCCGTAGAGATGCC 310

Qy   318 CAGTAATTTCCTCCGTTGGGGTTCGGAGGCCACGGTCACCGTCTCCTCA 377
           ||||||||||||||| |||||||||||||||||||||||||||||||
Db   311 TACAATTTTTAGAAACATCCAATCGGGGGGGATGCCTTTGATATCTGGGGCCAAGGGACAAT 370

Qy   378 GGTCATCGTCTCCTCA 393
           |||| |||||||||||
Db   371 GGTCACCGTCTCCTCA 386

RESULT 18
LOCUS   AF466106   384 bp   DNA   linear   PRI 18-SEP-2002
DEFINITION Homo sapiens immunoglobulin heavy chain variable region gene,
            partial cds.
ACCESSION   AF466106
VERSION   AF466106.1 GI:18496730
KEYWORDS   .
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 384)
AUTHORS   Zhu,D., Orchard,J., Oscier,D.G., Wright,D.H. and Stevenson,F.K.
TITLE   V(H) gene analysis of splenic marginal zone lymphomas reveals
            diversity in mutational status and initiation of somatic mutation
            in vivo
JOURNAL   Blood 100 (7), 2659-2661 (2002)
MEDLINE   22224400
PUBMED   12239182
REFERENCE   2 (bases 1 to 384)
AUTHORS   Zhu,D., Orchard,J., Oscier,D.G., Wright,D.H. and Stevenson,F.K.
TITLE   Direct Submission
JOURNAL   Submitted (08-JAN-2002) Molecular Immunology Group, Tenovus
            Laboratory, Cancer Sciences Division, University of Southampton,
            Tremona Road, Southampton SO16 6YD, UK
COMMENT   Ig VH sequence from SMZL; case ME.
FEATURES   Location/Qualifiers
     source   1..384
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /isolate="SMZL; case ME"
                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /tissue_type="blood"
     CDS   <1..>384
                     /codon_start=1
                     /product="immunoglobulin heavy chain variable region"
                     /protein_id="AAL74207.1"
                     /db_xref="GI:18496731"
                     /translation="EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKG
                     LEWVSISSSSSYIYADSVKGRFTISRDNAKNSLYLQMNRLRAEDTAVYYCARDLRP
                     TLRLGELSVAYYFDYWGQGTLVTVSS"
BASE COUNT   85 a   96 c   115 g   88 t
ORIGIN
Query Match   70.9%; Score 278.6; DB 9; Length 384;
Best Local Similarity   86.1%; Pred. No. 7.7e-79;
Matches 321; Conservative 0; Mismatches 49; Indels 3; Gaps 1;

Qy   24 GGTGGAGTCTGGGGGAGGCGTTGGTCAACCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC   83
           |||||||||| |||||||||| ||||| ||||||||||||||||||||||||||||||
Db   12 GGTGGAGTCTCGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC   71

Qy   84 CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG 143
           |||||||||||||||||||| ||| ||||| ||||||||||| |||||||||||||||
Db   72 CTCTGGATTCACCTTCAGTAGTTATAGCATGAAACTGGGTCCGCCAGGCTCCAGGGAAGGG 131

Qy   144 GCTGGAGTGGGTCTCATCCATTAGTAATAGTAATACTTACCATACGGCAGCAGACGCAGT 203
           ||||||||||||||| |||||||||||| || || | | ||| |||||||||||||||||
Db   132 GCTGGAGTGGGTGTCATCCATTAGTAGTAGTAGTATTACTGGAGTCCGCGAGACTCAGT 191

Qy   204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
           ||||||||||||||||||||||||| |||||||||||||||||| |||||| ||||||||
Db   192 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 251

Qy   264 CAGCCTGAGAGCCGAGCACACGCGCTGTGTACTACTGTGCGAGAGATTCTAGATACAGTAA 323
           |||||||||||||||||||| ||| ||| |||||||||||| ||| ||| |||| | ||
Db   252 CCGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGATCTAAGGCCCACATT 311

Qy   324 TTTCCTCCGTTGGGGTTCGGAGGCCG--ACGGTATGGACGGTCTGGGCCGGGACCACGGT 380
           | || ||| |||||| |||||| |||| | |||| ||||||||
Db   ...

RESULT 19

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Db   312 ACGTTTTGGGGGGGAGTTTATCGGTCCGGTACTACTTTGACTACTGGGGCCAGGGAACCCTGGT 371
Qy   381 CATCGTCTCCTCA 393
         |||||||||||||
Db   372 CACCGTCTCCTCA 384
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LOCUS       AF466107                 384 bp    DNA     linear   PRI 18-SEP-2002
DEFINITION  Homo sapiens immunoglobulin heavy chain variable region gene,
            partial cds.
ACCESSION   AF466107
VERSION     AF466107.1  GI:18496732
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 384)
  AUTHORS   Zhu,D., Orchard,J., Oscier,D.G., Wright,D.H. and Stevenson,F.K.
  TITLE     V(H) gene analysis of splenic marginal zone lymphomas reveals
            diversity in mutational status and initiation of somatic mutation
            in vivo
  JOURNAL   Blood 100 (7), 2659-2661 (2002)
   MEDLINE  22224400
   PUBMED   12239182
REFERENCE   2  (bases 1 to 384)
  AUTHORS   Zhu,D., Orchard,J., Oscier,D.G., Wright,D.H. and Stevenson,F.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-JAN-2002) Molecular Immunology Group, Tenovus
            Laboratory, Cancer Sciences Division, University of Southampton,
            Tremona Road, Southampton SO16 6YD, UK
COMMENT     Ig VH sequence from SMZL; case ME.
FEATURES             Location/Qualifiers
     source          1..384
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /isolate="SMZL; case ME"
                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /tissue_type="spleen"
     CDS             <1..384
                     /codon_start=1
                     /product="immunoglobulin heavy chain variable region"
                     /protein_id="AAL74208.1"
                     /db_xref="GI:18496733"
                     /translation="EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKG
                     LEWVSISSSSSYIYADSVKGRFTISRDNAKNSLYLQMNRLRAEDTAVYYCARDLRP
                     TRLGELSVAYFDYWGQGTLVTVSS"
BASE COUNT       85 a    96 c   115 g    88 t
ORIGIN
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Query Match     70.9%;  Score 278.6;  DB 9;  Length 384;
Best Local Similarity   86.1%;  Pred. No. 7.7e-79;
Matches  321;  Conservative   0;  Mismatches  49;  Indels   3;  Gaps   1;
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Qy    24 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
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Db    12 GGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 71

Qy    84 CTCTGGATTCACCTTCAGTAGCTATAGCAATGCATGGGTCCGCCAGGCTCCAGGGAAGGG 143
         |||||||||||||||||||| ||||  ||| |  |||||| |||||| ||||||||||||
Db    72 CTCTGGATTCACTTTCAGTAGTTATTATAGGCCCAGGGTTCCAGGGAAGGG         131

Qy   144 GCTGGAGTGGGTCTCATCTATTAGTAATAATAGTAATAACATTATACATTATACGCAGACTCCGAGT 203
         ||||||||||||||||||||||||| ||||  ||||||| |  ||  |||||||||||||| ||||
Db   132 GCTGGAGTGGGTCTCATCCATTAGTAGTAGTAGTTACATATTACGCAGACTCAGT         191

Qy   204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   192 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 251
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RESULT 20

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Qy   264 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGATTCTAGATACAGTAA 323
         |||| ||||||||||||||||||||||||||||||||| |||| |||||||| ||||||| |
Db   252 CCGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATTCTAAGGCCCACATT 311

Qy   324 TTTCCTCCGTTCGGTTCGGAGCG---ACCGTATCGGAGCGTCTGGGGCCAAGGGACCACGGT 380
         ||||||| | |||||  ||||||   |||||||||||||||||||||||||||||||||| ||
Db   312 ACGTTTTGGGGGGGAGTTTATCGGTCCGGTACTACTTTGACTACTGGGGCCAGGGAACCCTGGT 371

Qy   381 CATCGTCTCCTCA 393
         |||||||||||||
Db   372 CACCGTCTCCTCA 384
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LOCUS       HSROU221                 441 bp    mRNA    linear   PRI 29-FEB-1996
DEFINITION  H.sapiens rearranged VDJ region (ROU221).
ACCESSION   X81751
VERSION     X81751.1  GI:1209423
KEYWORDS    diversity region; immunoglobulin heavy chain; joining region;
            variable region; VH-3 family.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Milili,M., Schiff,C., Fougereau,M. and Tonnelle,C.
  TITLE     The VDJ repertoire expressed in human preB cells reflects the
            selection of bona fide heavy chains
  JOURNAL   Eur. J. Immunol. 26.(1), 63-69 (1996)
   MEDLINE  96152725
   PUBMED   8566085
REFERENCE   2  (bases 1 to 441)
  AUTHORS   Tonnelle,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-SEP-1994) C. Tonnelle, Centre d'Immunologie
            Marseille-Luminy, Case 906, 13288 Marseille, Cedex 9, FRANCE
COMMENT     Related sequences: X65741, X65883 to X65920.
FEATURES             Location/Qualifiers
     source          1..441
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /clone="ROU 221"
                     /cell_type="pre B-lymphocytes"
                     /tissue_type="bone marrow"
                     /clone_lib="ROU"
                     /rearranged
     sig_peptide     1..57
     V_region        58..353
                     /product="immunoglobulin heavy chain V region"
     D_segment       354..389
                     /product="immunoglobulin heavy chain D segment"
     J_segment       390..441
                     /product="immunoglobulin heavy chain J segment"
BASE COUNT       98 a    94 c   134 g   115 t
ORIGIN
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Query Match     70.9%;  Score 278.6;  DB 9;  Length 441;
Best Local Similarity   86.1%;  Pred. No. 7.9e-79;
Matches  321;  Conservative   0;  Mismatches  49;  Indels   3;  Gaps   1;
```

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Qy    24 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    24 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83

Qy    84 CTCTGGATTCACCTTCAGTAGCTATAGCAATGCATGGGTCCGCCAGGCTCCAGGGAAGGG 143
         ||||||||||||||||||||  |||||| || | ||| ||||||||||||||||||||||
Db    84 CTCTGGATTCACCTTCAGTAGCTATAGCACAGGGTTGGGTCCGCCAGGCTCCAGGGAAGGG 143

Qy   144 GCTGGAGTGGGTCTCATCCATTAGTAATAATAGTAATAACATTATACATTATACGCAGACTCCGCAGT 203
         |||||||||||||||| |||||||  |||  ||||||  ||| |  |||  |||| || |||| |
Db   129 CTCTGGATTCACCTTCAGTAGTTATGAAATGAACTGGGTCCGCCAGGCTCCAGGGAAGGG 188
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Db    189  GCTGGAGTGGGTTTCATACATTAGTAGTAGTGGTAGTACCATATACTACGCAGACTCTGT  248

Qy    204  GAAGGGCCGATTCACCAATCTCCAGAGACAAACGCCAAGAACTCACTGTATCTGCAAAATGAA  263
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    249  GAAGGGCCGATTCACCAATCTCCAGAGACAAACGCCAAGAACTCACTGTATCTGCAAAATGAA  308

Qy    264  CAGCCTGAGAGCCGAGCACACGGCCTGTGTTACTACTGTGCGAGAGATTCTAGATACAGTAA  323
           |||||||||||||||||||||||||| ||||||||||| | |             |    |
Db    309  CAGCCTGAGAGCCGAGGACACGGGCTGTTTATTACTGTGCCGAGAGACCGGAAGTATTACGA  368

Qy    324  TTTTCCTCCGTTGGGGTTCGGA---GCGACGGTATGGACGTTCTGGGGCCCAAGGGACCACGGT  380
           ||  |  ||| | |  ||        |||||||||||||||||||||||||||||||
Db    369  TTTTTGGAGTGGTTTATTATAATCTACTACGGTATGGACGTTCTGGGGCCCAAGGGACCACGGT  428

Qy    381  CATCGTCTCCCTCA  393
           || |||||||||||
Db    429  CACCGTCTCCCTCA  441
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2003, 22:34:02 ; Search time 269 Seconds
               (without alignments)
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                                        GenCore version 5.1.6
                                        Copyright (c) 1993 - 2003 Compugen Ltd.

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Perfect score: 393
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Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 60 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	DB	ID	Description
1	393	100.0	393	22	AAH68642	Human anti-Rh(D) c
2	363.6	92.5	381	22	AAH68641	Human anti-Rh(D) c
3	272.2	69.3	311	23	ABS46318	Human liver single
4	272.2	69.3	311	24	ABS20923	Human genome-deriv
5	272.2	69.3	519	16	AAQ78959	Human immunoglobul
6	271.8	69.2	375	22	AAF29047	Human immunoglobu
7	269.6	68.6	348	24	AAD46290	Human HIV-1 monocl
8	269.6	68.6	348	24	AAD46292	Human KDR (VEGFR-

9	269.6	68.6	348	25	ABT23325	VEGF binding relat
10	269.6	68.6	348	25	ABT23327	VEGF binding relat
11	268.8	68.4	376	24	ABS62722	Anti-IGF-IR antibo
12	268	68.2	348	24	AAD46294	Human KDR (VEGFR-2
13	268	68.2	348	25	ABT23329	VEGF binding relat
14	268	68.2	458	22	AAH41153	Human coding seque
15	261.6	66.6	376	24	ABS62704	Anti-IGF-IR antibo
16	261.2	66.5	381	20	AAX77236	Human D4.5 heavy c
17	261.2	66.3	414	19	AAV68537	Nucleotide sequenc
18	260.2	66.2	1630	21	AAZ50587	HD70scFv-CH1-GM-CS
19	260.2	66.2	1630	21	AAZ50588	HD70scFv-CH1-Inter
20	260.2	66.2	1630	21	ABK43226	IgG antibody 2.1.1
21	260	66.0	816	21	AAA46898	DNA encoding the h
22	259.2	65.9	1413	20	AAS03516	DNA encoding anti-
23	258.8	65.6	381	22	AAO78986	Human immunoglobul
24	257.2	65.4	402	18	AAT43529	DNA encoding anti-
25	255	64.9	375	24	ABL53509	Variable heavy cha
26	253.6	64.5	376	15	AAO66539	Human immunoglobu
27	253.2	64.4	429	24	AAH62700	Anti-IGF-IR antibo
28	252.8	64.3	437	24	ABS62700	Human recombinant
29	252.8	64.3	375	24	AAA46886	Human PTHrP monocl
30	252	64.1	562	21	AAV49460	Anti-IGF-IR antibo
31	251.6	63.9	429	21	AAA13939	Human PTHrP monocl
32	251	63.8	762	19	AAH47732	cDNA encoding huma
33	250.6	63.8	357	22	ABZ22308	Human PTHrP monocl
34	250.4	63.7	474	25	ABT31879	Anti-CD40 monoclon
35	250.4	63.7	520	21	AAA13936	S. pneumoniae PPS-
36	250	63.6	429	21	AAA13936	Human PTHrP monocl
37	249	63.4	354	22	AAS03470	DNA encoding anti-
38	248.8	63.3	375	25	AB224184	Anti-EGFR antibody
39	248.8	63.3	456	11	AAQ03610	Sequence encoding
40	248.8	63.2	429	21	AAA13930	Human PTHrP monocl
41	248.4	63.2	429	21	AAA13931	Human PTHrP monocl
42	248.4	63.2	429	21	AAA13932	Human PTHrP monocl
43	248.4	63.2	429	21	AAA13933	Human PTHrP monocl
44	248.4	63.2	429	21	AAA13937	Human PTHrP monocl
45	248.4	63.2	1458	22	AAS22625	Human recombinant
46	247.6	63.0	527	24	ABL65878	Lung cancer relate
47	247.6	63.0	527	24	ABL67549	Thyroid cancer rel
48	247.2	62.9	375	11	AAQ03608	Sequence encoding
49	246.8	62.8	354	22	AAC96948	Human anti-HBs ant
50	246.8	62.8	393	22	AAH47730	Nucleotide sequenc
51	246.8	62.8	418	24	ABS62724	Anti-IGF-IR antibo
52	245.8	62.5	715	16	AAQ78949	Human immunoglobul
53	245.6	62.5	437	24	ABL55510	Human recombinant
54	245.6	62.5	437	24	ABL55511	Human recombinant
55	245.6	62.5	4026	24	ABK81191	DNA encoding immun
56	245.4	62.4	1605	22	AAH18432	Human cDNA sequenc
57	245	62.3	296	24	AAS62711	Germline anti-IGF-
58	245	62.3	349	22	AAS03504	DNA encoding anti-
59	244.8	62.3	437	24	ABL53508	Human recombinant
60	244.4	62.2	372	20	AAV72230	Human anti-GP1Ib/I

ALIGNMENTS

RESULT 1
AAH68642

Left column:

```
XX
PD   03-JUL-2001.
XX
PF   29-JAN-1999;
XX
PR   99US-0240274.
XX
PR   96US-0028550.
PR   98US-0081380.
PR   27-JUN-1997;   97US-0084045.
XX
PA   (UYPE-) UNIV PENNSYLVANIA.
XX
PI   Siegel DL;
XX
PR   WPI; 2001-388931/41.
DR   P-PSDB; AAG93585.
XX
PS   Example 2; Column 53; 162pp; English.
XX
PT   New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT   diagnostics requiring a human instead of an animal antibody and in
PT   therapeutic medicine -
XX
CC   The present invention describes an isolated Rh(D) binding protein,
CC   preferably a human antibody, (I) having an amino acid sequence comprising
CC   one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC   immunostimulant activity, and can be used as an immune system stimulant.
CC   (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC   are used in diagnostics that require human antibodies instead of animal
CC   antibodies, such as determine the Rh phenotype of human red blood cells.
CC   AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC   AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC   chain CDR3 amino acid sequences which are given in the exemplification
CC   of the present invention.
XX
SQ   Sequence 393 BP; 88 A; 99 C; 120 G; 86 T; 0 other;

Query Match            100.0%;   Score 393;   DB 22;   Length 393;
Best Local Similarity  100.0%;   Pred. No. 4.4e-107;
Matches  393;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy         1 GAGGTGCAGCTGCTCGAGTCTGGGGGTGGAGTCGTGGGGGGAGGCCTGGTCAAGCCTGGGGGG    60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 GAGGTGCAGCTGCTCGAGTCTGGGGGTGGAGTCGTGGGGGGAGGCCTGGTCAAGCCTGGGGGG    60

Qy        61 TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATAGCACTGG   120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATAGCACTGG   120

Qy       121 GTCCGCCAGGGTCCAGGGAAGGGGCTGGAGTGGGTCTCATCCATTAGTAATAGTAATATACT   180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 GTCCGCCAGGGTCCAGGGAAGGGGCTGGAGTGGGTCTCATCCATTAGTAATAGTAATATACT   180

Qy       181 TACATATACTACCGCAGACGACGACGCCATTCACCATCTCCAGAGACAACGCCAAG   240
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Db       181 TACATATACTACCGCAGACGACGACGCCATTCACCATCTCCAGAGACAACGCCAAG   240

Qy       241 AACTCACTGTATCTGCAAAATGAACAGCCGAGAGCCGAGGACACGGCTGTGTTACTACTGT   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 AACTCACTGTATCTGCAAAATGAACAGCCGAGAGCCGAGGACACGGCTGTGTTACTACTGT   300

Qy       301 GCGAGAGATTCTAGATACAGTAATTCTCCTCCGTTGGGACGGGTATGGACGTC   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 GCGAGAGATTCTAGATACAGTAATTCTCCTCCGTTGGGACGGGTATGGACGTC   360

Qy       361 TGGGGCCAAGGGACCACGGTCATCGTCTCCCTCA   393
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Db       361 TGGGGCCAAGGGACCACGGTCATCGTCTCCCTCA   393
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RESULT 2
AAH68641
ID   AAH68641 standard; DNA; 381 BP.
XX
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Right column:

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AC   AAH68641;
XX
DT   14-SEP-2001 (first entry)
XX
DE   Human anti-Rh(D) chain E011s nucleotide sequence.
XX
KW   Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW   red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
XX
OS   Homo sapiens.
XX
PA   (UYPE-) UNIV PENNSYLVANIA.
XX
PN   Siegel DL;
XX
PN   US6255455-B1.
XX
PD   03-JUL-2001.
XX
PF   29-JAN-1999;   99US-0240274.
XX
PR   96US-0028550.
PR   98US-0081380.
PR   27-JUN-1997;   97US-0084045.
XX
DR   WPI; 2001-388931/41.
DR   P-PSDB; AAG93584.
XX
PS   Example 2; Column 53; 162pp; English.
XX
PT   New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT   diagnostics requiring a human instead of an animal antibody and in
PT   therapeutic medicine -
XX
CC   The present invention describes an isolated Rh(D) binding protein,
CC   preferably a human antibody, (I) having an amino acid sequence comprising
CC   one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC   immunostimulant activity, and can be used as an immune system stimulant.
CC   (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC   are used in diagnostics that require human antibodies instead of animal
CC   antibodies, such as determine the Rh phenotype of human red blood cells.
CC   AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC   AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC   chain CDR3 amino acid sequences which are given in the exemplification
CC   of the present invention.
XX
SQ   Sequence 381 BP; 98 A; 113 G; 83 T; 0 other;

Query Match            92.5%;   Score 363.6;   DB 22;   Length 381;
Best Local Similarity  98.9%;   Pred. No. 2.5e-98;
Matches  366;   Conservative   0;   Mismatches   4;   Indels   0;   Gaps   0;

Qy        24 GCTGGAGTCTGGGGGGAGGCCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC    83
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Db        12 GCTGGAGTCTGGGGGGAGGCCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC    71

Qy        84 CTCTGGATTCACCTTCAGTAGCTATAGCACTGGGTCCCCAGGGTCCAGGGAAGGG   143
             ||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        72 CTCTGGATTCACCTTCAGTAGCTATAGCACTGGGTCCCCAGGGTCCAGGGAAGGG   131

Qy       144 GCTGGAGTGGGTCTCATCCATTAGTAATAGTAATAGTAATACTTACATATTACTACGGAGACCCGAGT   203
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Db       132 GCTGGAGTGGGTCTCATCCATTAGTAATAGTAATAGTAATACTTACATATTACTACGGAGACCCGAGT   191

Qy       204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAAATGAA   263
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Db       192 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAAATGAA   251

Qy       264 CAGCCTGAGAGCCGAGGACACGGCTGTGTTACTACTGTGCGAGAGATTCTAGATACAGTAA   323
             |||||||||||||||||||||||||||||||||||| ||||||||||| ||||
Db       252 CAGCCTGAGAGCCGAGGACACGGCTGTGTTACTACTGTGCGAGAGATTCTAGATACAGTAA   311

Qy       324 TTTCCTCCGTTGGGTTCGGGACGGGCCACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCAT   383
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Db           ...
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Db    312 TTTCCTCCGTTGGGTTCGGACGACGGTATGGACGTGTCGGGGCCAAGGGACCACGGTCAT
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                                                     CAT 371
Qy    384 CGTCTCCTCA 393
          ||||||||||
Oy    372 CGTCTCCTCA 381
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RESULT 3
AB546318

ID   AB546318 standard; DNA; 311 BP.
XX
AC   AB546318;
XX
DT   25-FEB-2003 (first entry)
XX
DE   Human liver single exon nucleic acid probe, SEQ ID NO 21308.
XX
KW   Human; single exon nucleic acid probe; liver; cirrhosis;
KW   hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
KW   coronary heart disease; ss.
XX
OS   Homo sapiens.
XX
XX
PN   WO20015727-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00664.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0633266.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR   WPI; 2001-488898/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analysing gene expression in human adult liver -
XX
PS   Claim 4; SEQ ID NO 21308; 658pp; English.
XX
CC   The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC   measuring human gene expression in a sample derived from human adult
CC   liver, comprising one of 13109 defined nucleotide sequences given in the
CC   specification (or complements/ fragments). The probe hybridises at high
CC   stringency to a nucleic acid molecule expressed in the human adult
CC   liver. (I) may be used for predicting, measuring and displaying gene
CC   expression in samples derived from human adult liver. The genes
CC   identified may be involved in genetic liver diseases such as cirrhosis,
CC   hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which
CC   is associated with coronary heart disease. ABS25011-ABS51005 represent
CC   human liver single exon nucleic acid probes of the invention.
CC   Note: The sequence information for this patent does not appear in the
CC   printed specification but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 311 BP; 73 A; 75 C; 96 G; 67 T; 0 other;

Query Match   69.3%; Score 272.2; DB 23; Length 311;
Best Local Similarity 97.2%;
Matches 277; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```
Qy   24 GGTGGAGTCTGGGGAGGGGAGGGCCTGGTCAAGGCCTGGGGTCCCTGAGACTCTCCTGTGCCAGC 83
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   23 GGTGGAGTCTGGGGAGGGGAGGGCCTGGTCAAGGCCTGGGGTCCCTGAGACTCTCCTGTGCCAGC 82
```

```
Qy   84 CTCTGGATTCACCTTCAGTTAGCTYATAGCATGCACTGGGGTCCGCCGCCAGGGGTCCAGGGAAGGG 143
         ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   83 CTCTGGATTCACCTTCAGTTAGCGTATAGCATGCACTGGGGTCCGCCGCCAGGGGTCCAGGGAAGGG 142

Qy  144 GCTGGAGTGGGGTCGTCATCACCATTAGTAATAGTAATACATATAATACTACGGCAGACGCAGT 203
         |||||||||||| |||||||| ||||||||||||||||||||||||||||||||||||||||||
Db  143 GCTGGAGTGGGGTCGTCATCCATTAGTAATAGTAATACATATAATACTACGGCAGACGCAGT 202

Qy  204 GAAGGGCCGGATTCACCACTCTCCAGAGAGAACAAGGCCAAGAACTCACTGTATCTGCAAATGAA 263
         |||||||||||||||||| ||||||||| |||||||||||||||||||||||||||||||||||
Db  203 GAAGGGCCGGATTCACCATTCCAGAGACAACAAGGCCAAGAACTCACTGTATCTGCAAATGAA 262

Qy  264 CAGCCTGAGAGCCGAGCACACGGCTGTGTGTACTACTGTGTCCGAGAGA 308
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  263 CAGCCTGAGAGCCGAGCACACGGCTGTGTATTACTGTGTCCGAGAGA 307
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RESULT 4
AB520923

ID   AB520923 standard; DNA; 311 BP.
XX
AC   AB520923;
XX
DT   19-AUG-2002 (first entry)
XX
DE   Human genome-derived single exon probe ORF from lung SEQ ID NO 20914.
XX
KW   Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
KW   chronic obstructive pulmonary disease; interstitial lung disease;
KW   familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW   tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW   Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW   pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome;
KW   pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW   primary ciliary dyskinesis; pulmonary hypertension;
KW   hyaline membrane disease; open reading frame; ORF.
XX
OS   Homo sapiens.
XX
XX
PN   WO200186003-A2.
XX
PD   15-NOV-2001.
XX
PF   30-JAN-2001; 2001WO-US00665.
XX
PR   04-FEB-2000; 2000US-180312P.
PR   26-MAY-2000; 2000US-207456P.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-234687P.
PR   27-SEP-2000; 2000US-236359P.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR   WPI; 2002-114183/15.
XX
PT   Spatially-addressable set of single exon nucleic acid probes, used to
PT   measure gene expression in human lung samples -
XX
PS   Claim 4; SEQ ID NO 20914; 634pp; English.
XX
CC   The invention relates to a spatially-addressable set of single exon
CC   nucleic acid probes for measuring gene expression in a sample derived
CC   from human lung comprising single exon nucleic acid probes having one of
CC   12614 nucleic acid sequences mentioned in the specification, or their
CC   complements or the 12287 open reading frames derived from the 12614
CC   probes. Also included are a microarray comprising the novel set of
CC   probes; the novel set of probes which hybridise at high stringency to a
CC   nucleic acid expressed in the human lung; measuring gene expression in a

```
CC   sample derived from human lung, comprising (a) contacting the array with
CC   a collection of detectably labeled nucleic acids derived from human lung
CC   mRNA, and (b) measuring the label detectably bound to each probe of the
CC   the array; identifying exons in a eukaryotic genome, comprising
CC   (a) algorithmically predicting at least one exon from genomic sequences
CC   of the eukaryote; and (b) detecting specific hybridisation of detectably
CC   labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC   having a fragment identical to the predicted exon, the probe is included
CC   in the above mentioned microarray; assigning exons to a single gene,
CC   comprising (a) identifying exons from genomic sequence by the method
CC   above and (b) measuring the expression of each of the exons in several
CC   tissues and/or cell types using hybridisation to a single exon
CC   microarrays having a probe with the exon, where a common pattern of
CC   expression of the exons in the tissues and/or cell types indicates that
CC   the exons should be assigned to a single gene; a peptide comprising one
CC   of 12011 sequences, mentioned in the specification, or encoded by the
CC   probes/open reading frames (ORF). The probes are used for gene
CC   expression analysis, and for identifying exons in a gene, particularly
CC   using human lung derived mRNA and for the study of lung diseases
CC   such as asthma, lung cancer, chronic obstructive pulmonary disease
CC   (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
CC   fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
CC   Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
CC   haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis,
CC   pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic
CC   pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension
CC   and hyaline membrane disease. The present sequence is a single exon
CC   probe open reading frame of the invention.
CC   Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic
CC   format directly from WIPO at:
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 311 BP; 73 A; 75 C; 96 G; 67 T; 0 other;
XX

Query Match   69.3%;  Score 272.2;  DB 24;  Length 311;
Best Local Similarity  97.2%;  Pred. No. 3.8e-71;
Matches  277;  Conservative  0;  Mismatches  8;  Indels  0;  Gaps  0;

Qy         24 GGTGGAGTCTGGGGGAGGACGGCCTGGTCAAGCCTGGGGGGGGTCCCTGAGAGTCTCCTGTGTGCAGC  83
              ||||||||||||||||||||||||||||||||||||||||||| |||||||| |||||| ||||||||
Db         23 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGGGTCCCTGGGGACTCTCCTGTGCAGC  82

Qy         84 CTCTGGATTCACCTTCAGTAGCTATAGACATCCACTGGGTCCGCCAGGGTCCAGGGAAGG  143
              |||||||||||||||||||||||||||| |||||||||||| |||||||||||||||||||
Db         83 CTCTGGATTCACCTTCAGTAGCTATAGCATGAACTGGGTCCGCCAGGCTCCAGGGAAGG  142

Qy        144 GCTGGAGTGGGGTTCTCATCCATTAGTAATAGTAAATACTTACATATACTACCGCAGACGGCCAGT  203
              |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db        143 GCTGGAGTGGGGTTCTCATCCATTAGTAGTAGTTACACATATACTACCGCAGACTCAGT  202

Qy        204 GAAGGGCCGATTCACCATCTCCAGAGACAAACGCCAAGAACTCACTGTATCTGCAAATGAA  263
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        203 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA  262

Qy        264 CAGCCTGAGAGCCGACACACGGCCGTGTATTACTGTGCGAGAGA  307
              ||||||||||||||||||||||||||||||||||||||||||||
Db        263 CAGCCTGAGAGCCGACACACGGCCGTGTATTACTGTGCGAGAGA  307
```

```
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT
FT   CDS             11..462
FT                   /*tag= a
FT                   /product= human immunoglobulin variable heavy chain
FT   intron          57..157
FT                   /*tag= b
FT   misc_signal     463..465
FT                   /*tag= c
FT                   /note= "miscellaneous signal, does not conform to
FT                   termination or splice site sequence"
XX
PN   WO9426895-A1.
XX
PD   24-NOV-1994.
XX
PF   10-MAY-1993; 93WO-JP00603.
XX
PR   10-MAY-1993;  93WO-JP00603.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
PI   Honjo T, Matsuda F;
DR   WPI; 1995-006791/01.
DR   P-PSDB; AAR66313.
XX
PT   A series of genes (AAO78939-79002) encoding human immunoglobulin
PT   variable heavy chains. The genes were isolated and cloned from a series
CC   of cosmid constructs: Y202; Y103; Y21; Y6;Y24; 3-31; M84; M118 and M131,
CC   by PCR amplification using primers AAO78917-38. The genes are subdivided
CC   into 5 families of Vh genes. The fragments cover a region of 800 kb.
CC   The DNA fragments were isolated from high molecular weight DNA from
CC   human placenta. The DNA was partially digested with TaqI restriction
CC   enzyme. The fragments were separated by gel electrophoresis and 35-45 kb
CC   fractions were collected. The fragments were ligated with ClaI-digested
CC   cosmid vector pJB81. The ligation products were in vitro packed and
CC   infected into E.coli 490A. The fragments were then subcloned by colony
CC   hybridisation. The Vh genes and the DNA fragments encoding them are
CC   useful in producing human immunoglobulin in mammalian hosts.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 519 BP; 123 A; 111 C; 161 G; 124 T; 0 other;
XX

Query Match   69.3%;  Score 272.2;  DB 16;  Length 519;
Best Local Similarity  97.2%;  Pred. No. 4.5e-71;
Matches  277;  Conservative  0;  Mismatches  8;  Indels  0;  Gaps  0;

Qy         24 GGTGGAGTCTGGGGGAGGACGGCCTGGTCAAGCCTGGGGGGGGTCCCTGAGAGTCTCCTGTGTGCAGC  83
              ||||||||||||||||||||||||||||||||||||||||||| |||||||| |||||| ||||||||
Db         84 CTCTGGATTCACCTTCAGTAGCTATAGCATGAACTGGGTCCGCCAGGCTCCAGGGAAGG  143

Qy         84 CTCTGGATTCACCTTCAGTAGCTATAGACATCCACTGGGTCCGCCAGGGTCCAGGGAAGG  143
              |||||||||||||||||||||||||||| |||||||||||| |||||||||||||||||||
Db        180 GGTGGAGTGGGGTTCTCATCCATTAGTAGTAGTTACACATATACTACCGCAGACTCAGT  239

Qy        144 GCTGGAGTGGGGTTCTCATCCATTAGTAATAGTAAATACTTACATATACTACCGCAGACGGCCAGT  203
              |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db        240 CTCTGGATTCACCTTCAGTAGCTATAGCATGAACTGGGTCCGCCAGGCTCCAGGGAAGG  299

Qy        204 GAAGGGCCGATTCACCATCTCCAGAGACAAACGCCAAGAACTCACTGTATCTGCAAATGAA  263
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        300 GCTGGAGTGGGGTTCTCATCCATTAGTAGTAGTTACACATATACTACCGCAGACTCAGT  359

Qy        204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA  263
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        360 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA  419

Qy        264 CAGCCTGAGAGCCGACACACGGCCGTGTATTACTGTGCGAGAGA  308
              ||||||||||||||||||||||||||||||||||||||||||||
Db        264 CAGCCTGAGAGCCGACACACGGCCGTGTATTACTGTGCGAGAGA  308
```

```
RESULT 5
AAQ78959
ID   AAQ78959 standard; DNA; 519 BP.
XX
AC   AAQ78959;
XX
DT   25-MAR-2003 (updated)
DT   03-AUG-1995 (first entry)
XX
DE   Human immunoglobulin Vh gene #21.
XX
KW   Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
KW   cosmid; placenta; vector; pJB81; E.coli; mammalian; ds.
```

DNA fragment comprising human immunoglobulin Vh genes - for the
production of human immunoglobulin in mammalian hosts

Claim 30; Page 57-58; 130pp; Japanese.

```
Db      420 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGA 464
```

```
Qy      318 TGGCTACT---------CCTACGGTGTGGACGTCTGGGGCCAAGGGACCACGGGTCACCGT 368
               ||||||| |             | |||| ||||||||||||||||||||||||||||||||||||

Db      369 CTCCTCA 375
```

RESULT 6
AAF29047

ID   AAF29047 standard; DNA; 375 BP.
XX
AC   AAF29047;
XX
DT   03-APR-2001 (first entry)
XX
DE   Human HIV-1 monoclonal antibody coding sequence SEQ ID NO: 3.
XX
KW   Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
KW   envelope glycoprotein; gp120; diagnosis; ds.
XX
OS   Homo sapiens.
XX
PN   WO20010678-A1.
XX
PD   04-JAN-2001.
XX
PF   23-JUN-2000; 2000WO-US17327.
XX
PR   30-JUN-1999; 99US-0141701.
XX
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Watkins BA, Reitz MS;
XX
DR   WPI; 2001-112438/12.
DR   P-PSDB; AAB62746.
XX
CC   These can be used in diagnosis and therapy of HIV-1 infection.
CC   with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
CC   variable regions of human monoclonal antibodies which are immunoreactive
CC   The present invention provides the protein and coding sequences for the
XX
PS   Claim 4; Page 35; 81pp.
XX
PT   infected mammal.
PT   in biological sample and providing passive immunotherapy to HIV-1
PT   immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
PT   Novel human monoclonal antibody immunoreactive with human
XX

SQ   Sequence 375 BP; 83 A; 96 C; 113 G; 83 T; 0 other;

```
Query Match             69.2%;   Score 271.8;  DB 22;  Length 375;
Best Local Similarity   86.1%;   Pred. No. 5.3e-71;
Matches  316;  Conservative    0;  Mismatches   42;  Indels    9;  Gaps   1;
```

```
Qy       27 GGAGTCTGGGGGAGGCCGGTGGCTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTC 86
            ||||| || ||||||||| ||| |||||| ||||||||||||||||| ||||||| ||||||
Db       18 GGAGTCGGGGGGAGGCCTTGGTACAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTC 77

Qy       87 TGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGGGCT 146
            ||||||| |||||||| ||||||| || |||||||||||||||||||| ||||| ||||||
Db       78 TGGATTCACCTTCAGTACCTACAGCATGAACTGGGTCCGCCAGGCTCCAGGGAAGGGGCT 137

Qy      147 GGAGTGGGGTCTCATCCATTAGTAGTAATAGTAATACTTACATATAATACGGCAGACCGAGTGAA 206
            |||||||| || || |||| |||| | | |||||| |   | ||| ||||| | ||||| ||||||
Db      138 GGAGTGGATTTCATTACATTACCTAGTAGTGGTAGTCCCATATACTACCGGAGACTCGTGAA 197

Qy      207 GGGCCGAATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAACAG 266
            |||||||||| |||||| |||||||| | ||| |||| ||||||| |||||| ||||||||
Db      198 GGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAACAG 257

Qy      267 CCTGAGAGCCGAGCACACGGCTGTGTATTACTGTGCGAGAGATTCTAGATACAGTAATTT 326
            ||||||||| || |||| ||| || ||||||||| | | |  ||||||  ||||| ||
Db      258 CCTGAGACCGAGGACACGGCTGTGTATTACTGTGCGAGAGATTTAAGTGGGTGGCCATCTT 317

Qy      327 CCTCCGTTGGGGTTCGGAGGACGGTATGGACGTCTGGGGCCAAGGGACCACGGGTCATCGT 386
            |  | |||| ||||||||||||| ||||||||||||||||||||||||||||||||||||| |||
```

RESULT 7
AAD46290

ID   AAD46290 standard; DNA; 348 BP.
XX
AC   AAD46290;
XX
DT   27-DEC-2002 (first entry)
XX
DE   Human KDR (VEGFR-2) Fab heavy chain (VH) DNA from D2C6 clone.
XX
KW   Human; tumour; vascular endothelial growth factor receptor; metastasis;
KW   epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC;
KW   breast; VEGFR; heart; EGFR; therapy; invasiveness; heavy chain; gene;
KW   VH; ds.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FH
FT   CDS   1..348
FT   /*tag= a
FT   /product= "Human KDR (VEGFR-2) Fab heavy chain (VH)
FT   protein"
FT   /note= "CDS does not include start and stop codon"
FT   /partial
XX
PN   WO200270008-A1.
XX
PD   12-SEP-2002.
XX
PF   04-MAR-2002; 2002WO-US06762.
XX
PR   02-MAR-2001; 2001US-0798689.
XX
PA   (IMCL-) IMCLONE SYSTEMS INC.
PA   (ROCK/) ROCKWELL P.
PA   (GOLD/) GOLDSTEIN N I.
XX
PI   ROCKWELL P, GOLDSTEIN N I;
XX
DR   WPI; 2002-691738/74.
DR   P-PSDB; AAE28870.
XX
PT   antagonists.
PT   radiation, chemotherapeutic agents, or epidermal growth factor receptor
PT   endothelial growth factor receptor antagonists in combination with
PT   Inhibiting tumour growth in humans involves administering vascular
XX
PS   Example 9; Page 121-122; 151pp; English.
XX

CC   The invention relates to a method of inhibiting tumour growth which
CC   involves administering vascular endothelial growth factor receptor
CC   (VEGFR) antagonists in combination with radiation, chemotherapeutic
CC   agent, or epidermal growth factor receptor (EGFR) antagonist. The method
CC   is useful for inhibiting tumour growth in a human, where the tumour (e.g.
CC   tumour of the breast, heart, lung, small intestine, colon, spleen, bone,
CC   kidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin,
CC   bone marrow, blood, thymus, uterus, testicles, cervix or liver) over
CC   expresses VEGFR. It is also useful for inhibiting growth of colon tumour
CC   or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR.
CC   It is preferably useful for treating subjects with both solid tumours,
CC   preferably high vascular tumours and non-solid tumours. The inhibition
CC   or reduction of tumour growth includes prevention or inhibition of the
CC   progression of tumour, including cancerous and non-cancerous tumours,
CC   where the progression of tumours includes the invasiveness, metastasis,
CC   recurrence and increase in size of the tumour. The present sequence is
CC   human KDR (VEGFR-2) Fab antibody heavy chain DNA.
XX

SQ   Sequence 348 BP; 82 A; 85 C; 105 G; 76 T; 0 other;

Query Match
Best Local Similarity   68.8%;   Score 269.6;   DB 24;   Length 348;
Matches 275;   Conservative   0;   Mismatches   9;   Indels   0;   Gaps   0;

Qy   24 GGTGGAGTCTGGGGGAGGCCTGGTCCAAGCCTGGGGGTCCCTGAGACTCTCCTGTGTGCAGC 83
           |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   12 GGTTGCAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 71

Qy   84 CTCTGGGATTCACCTTCAGTAGCTATAGGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGG 143
           ||||||| || |||||||||||||||||||||| |||||||||||||||||||||||||||
Db   72 CTCTGGATTCACCTTCAGTAGCTATAGGCATGAACTGGGTCCCCCCAGGCTCCAGGGAAGG 131

Qy   144 GCTGGAGTGGGGTCTCATCCATTAGTAATAGTAATAACTTACATATACGCAGACGCAGT   203
           ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   132 GCTGGAGTGGGTCTCATCCATTAGTAGTAGTTACTAGTAGTTACATATACGCAGACGCAGT   191

Qy   204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA   263
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   192 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA   251

Qy   264 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG   307
           ||||||||||||||||||||||||||||||||||||||||||||
Db   252 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG   295

RESULT 8
AAD46292

ID   AAD46292   standard; DNA; 348 BP.
XX
AC   AAD46292;
XX
DT   27-DEC-2002   (first entry)
XX
DE   Human KDR (VEGFR-2) Fab heavy chain (VH) DNA from D1H4 clone.
XX
KW   Human; tumour; vascular endothelial growth factor receptor; metastasis;
KW   epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC;
KW   breast; VEGFR; heart; EGFR; therapy; invasiveness; heavy chain; gene;
KW   VH; ds.
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FH
FT   CDS   1..348
FT   /tag= a
FT   /product= "Human KDR (VEGFR-2) Fab heavy chain (VH)
FT   protein"
FT   /note= "CDS does not include start and stop codon"
FT   /partial
XX
PN   WO20027OO08-A1.
XX
PD   12-SEP-2002.
XX
PF   04-MAR-2002; 2002WO-US06762.
XX
PR   02-MAR-2001; 2001US-0798689.
XX
PA   (IMCL-) IMCLONE SYSTEMS INC.
PA   (ROCK/) ROCKWELL, P.
PA   (GOLD/) GOLDSTEIN N I.
XX
DR   WPI; 2002-691738/74.
DR   P-PSDB; AAE28870.
XX
PT   Inhibiting tumor growth in humans involves administering vascular
PT   endothelial growth factor receptor antagonists in combination with
PT   radiation, chemotherapeutic agents, or epidermal growth factor receptor
PT   antagonists -
XX
PS   Example 12; Page 124-125; 151pp; English.
XX

CC   The invention relates to a method of inhibiting tumour growth which
CC   involves administering, vascular endothelial growth factor receptor
CC   (VEGFR) antagonists in combination with radiation, chemotherapeutic
CC   agent, or epidermal growth factor receptor (EGFR) antagonist. The method
CC   is useful for inhibiting tumour growth in a human, where the tumour (e.g.
CC   tumour of the breast, heart, lung, small intestine, colon, spleen, bone,
CC   kidney, bladder, head and neck ovary, prostate, brain, pancreas, skin,
CC   bone marrow, blood, thymus, uterus, testicles, cervix or liver) over
CC   expresses VEGFR. It is also useful for inhibiting growth of colon tumour
CC   or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR.
CC   It is preferably useful for treating subjects with both solid tumours,
CC   preferably high vascular tumours and non-solid tumours. The inhibition
CC   or reduction of tumour growth includes prevention or inhibition of the
CC   progression of tumour, including cancerous and non-cancerous tumours,
CC   where the progression of tumours includes the invasiveness, metastasis,
CC   recurrence and increase in size of the tumour. The present sequence is
CC   human KDR (VEGFR-2) Fab antibody heavy chain DNA.
XX
SQ   Sequence 348 BP; 86 A; 104 C; 76 T; 0 other;

Qy   24 GGTGGAGTCTGGGGGAGGCCTGGTCCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGTGCAGC 83
           |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   12 GGTTGCAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 71

Qy   84 CTCTGGGATTCACCTTCAGTAGCTATAGGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGG 143
           ||||||| || |||||||||||||||||||||| |||||||||||||||||||||||||||
Db   72 CTCTGGATTCACCTTCAGTAGCTATAGGCATGAACTGGGTCCCCCCAGGCTCCAGGGAAGG 131

Qy   144 GCTGGAGTGGGGTCTCATCCATTAGTAATAGTAATAACTTACATATACGCAGACGCAGT   203
           ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   132 GCTGGAGTGGGTCTCATCCATTAGTAGTAGTTACTAGTAGTTACATATACGCAGACGCAGT   191

Qy   204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA   263
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   192 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA   251

Qy   264 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG   307
           ||||||||||||||||||||||||||||||||||||||||||||
Db   252 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG   295

RESULT 9
ABT23325

ID   ABT23325   standard; DNA; 348 BP.
XX
AC   ABT23325;
XX
DT   01-MAY-2003   (first entry)
XX
DE   VEGF binding related DNA SEQ ID NO 75.
XX
KW   Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;
KW   leukaemia cell; vascular endothelial growth factor; tumour;
KW   bispecific antigen-binding protein; human; gene; ds.
OS   Homo sapiens.
XX
PN   WO2003002144-A1.
XX
PD   09-JAN-2003.
XX
PF   26-JUN-2002; 2002WO-US20332.
XX
PR   26-JUN-2001; 2001US-30l299P.
XX
PA   (IMCL-) IMCLONE SYSTEMS INC.
XX
PI   Zhu Z;
XX

Column 1

```
DR   WPI; 2003-201468/19.
DR   P-PSDB; ABJ26763.
XX
PT   New bispecific antibodies having antigen-binding sites specific for a
PT   first vascular endothelial growth factor (VEGF) receptor and for a
PT   second VEGF receptor, useful for inhibiting migration of leukemia
PT   cells, or for treating tumors -
XX
PS   Disclosure; Page 70; 98pp; English.
XX
CC   The invention relates to a novel antibody having a first antigen binding
CC   site specific for a first vascular endothelial growth factor (VEGF)
CC   receptor and a second antigen-binding site specific for a second VEGF
CC   receptor. The bispecific antigen-binding proteins block activation of the
CC   VEGF receptor and are useful for reducing or inhibiting VEGF-induced
CC   cellular functions such as mitogenesis of vascular endothelial cells
CC   and migration of leukaemia cells. The antibodies are useful for treating
CC   tumours and for in vivo or in vitro for investigative and diagnostic
CC   methods. This polynucleotide sequence represents a human DNA sequence
CC   relating to the bispecific antibodies that bind to the VEGF receptors of
CC   the invention.
XX
SQ   Sequence 348 BP; 82 A; 85 C; 105 G; 76 T; 0 other;
XX
XX

Query Match      68.6%;   Score 269.6;   DB 25;   Length 348;
Best Local Similarity   96.8%;   Pred. No. 2.3e-70;
Matches  275;   Conservative   0;   Mismatches   9;   Indels   0;   Gaps   0;

Qy    24 GGTGGAGTCTGGGGAGGAGGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC  83
          ||||| ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db    12 GGTGCAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC  71

Qy    84 CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCAGGCAGGG  143
          |||||||||||||||||||||||||||||||| ||||||||||
Db    72 CTCTGGATTCACCTTCAGTAGCTATAGCATGAACTGGGTCCGCCAGGCTCCAGGGAAGGG  131

Qy   144 GCTGGAGTGGGTCTCAGTTATTAGTAATAGTAATAGTAATACTTACATACGCAGACGCAGT  203
          |||||||||||| ||| | || ||||| ||||||| |||| |||||| | ||||||| ||||
Db   132 GCTGGAGTGGGTGTCTCATCCATTAGTAGCTATAGCAATAGTAGTTACATATACTACGCAGACTCAGT  191

Qy   204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCAGTGTATCTGCAAATGAA  263
          ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db   192 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA  251

Qy   264 CAGCCTGAGAGCCGAGGACACGGCTGTGTACTACTGTGCGAGAG  307
          ||||||||||||||||||||||||||||||| ||||||||||||
Db   252 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG  295

RESULT 10
ID   ABT23327 standard; DNA; 348 BP.
XX
AC   ABT23327;
XX
DT   01-MAY-2003  (first entry)
XX
DE   VEGF binding related DNA SEQ ID No 79.
XX
KW   Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;
KW   leukaemia cell; vascular endothelial growth factor; tumour;
KW   bispecific antigen-binding protein; human; gene; ds.
XX
OS   Homo sapiens.
XX
XX   WO2003002144-A1.
XX
PD   09-JAN-2003.
XX
PN   WO2003002144-A1.
XX
PF   26-JUN-2002; 2002WO-US20332.
XX
PR   26-JUN-2001; 2001US-301299P.
XX
```

Column 2

```
PA   (IMCL-) IMCLONE SYSTEMS INC.
XX
PI   Zhu Z;
XX
DR   WPI; 2003-201468/19.
XX
PT   New bispecific antibodies having antigen-binding sites specific for a
PT   first vascular endothelial growth factor (VEGF) receptor and for a
PT   second VEGF receptor, useful for inhibiting migration of leukemia
PT   cells, or for treating tumors -
XX
PS   Disclosure; Page 72; 98pp; English.
XX
CC   The invention relates to a novel antibody having a first antigen binding
CC   site specific for a first vascular endothelial growth factor (VEGF)
CC   receptor and a second antigen-binding site specific for a second VEGF
CC   receptor. The bispecific antigen-binding proteins block activation of the
CC   VEGF receptor and are useful for reducing or inhibiting VEGF-induced
CC   cellular functions such as mitogenesis of vascular endothelial cells
CC   and migration of leukaemia cells. The antibodies are useful for treating
CC   tumours and for in vivo or in vitro for investigative and diagnostic
CC   methods. This polynucleotide sequence represents a human DNA sequence
CC   relating to the bispecific antibodies that bind to the VEGF receptors of
CC   the invention.
XX
SQ   Sequence 348 BP; 82 A; 86 C; 104 G; 76 T; 0 other;
XX
XX

Query Match      68.6%;   Score 269.6;   DB 25;   Length 348;
Best Local Similarity   96.8%;   Pred. No. 2.3e-70;
Matches  275;   Conservative   0;   Mismatches   9;   Indels   0;   Gaps   0;

Qy    24 GGTGGAGTCTGGGGAGGAGGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC  83
          ||||| ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db    12 GGTGCAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC  71

Qy    84 CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCAGGCAGGG  143
          |||||||||||||||||||||||||||||||| ||||||||||
Db    72 CTCTGGATTCACCTTCAGTAGCTATAGCATGAACTGGGTCCGCCAGGCTCCAGGGAAGGG  131

Qy   144 GCTGGAGTGGGTCTCAGTTATTAGTAATAGTAATAGTAATACTTACATACGCAGACGCAGT  203
          |||||||||||| ||| | || ||||| ||||||| |||| |||||| | ||||||| ||||
Db   132 GCTGGAGTGGGTGTCTCATCCATTAGTAGCTATAGCAATAGTAGTTACATATACTACGCAGACTCAGT  191

Qy   204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCAGTGTATCTGCAAATGAA  263
          ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db   192 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA  251

Qy   264 CAGCCTGAGAGCCGAGGACACGGCTGTGTACTACTGTGCGAGAG  307
          ||||||||||||||||||||||||||||||| ||||||||||||
Db   252 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG  295

RESULT 11
ID   ABS62722 standard; DNA; 376 BP.
XX
AC   ABS62722;
XX
DT   24-OCT-2002  (first entry)
XX
DE   Anti-IGF-IR antibody VH chain DNA consensus sequence #1.
XX
KW   Insulin-like growth factor I receptor; antibody; human; ds; gene;
KW   cytostatic; osteopathic; antiatherosclerotic; antipsoriatic;
KW   IGF-IR; tumour; anti-neoplastic; anti-tumour; anti-angiogenic;
KW   neuropathy; osteoporosis; acromegaly; gigantism; psoriasis;
KW   atherosclerosis.
XX
OS   Homo sapiens.
XX
XX   WO200253596-A2.
XX
PD   11-JUL-2002.
```

```
XX
PF   20-DEC-2001; 2001WO-US51113.
XX
PR   05-JAN-2001; 2001US-259927P.
XX
PA   (PFIZ ) PFIZER INC.
PA   (ABGE-) ABGENIX INC.
XX
PI   Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;
XX
DR   WPI; 2002-575410/61.
XX
PN   Novel humanized, chimeric monoclonal antibody that specifically binds
PT   to insulin-like growth factor I (IGF-I) receptor useful for inhibiting
PT   binding of IGF-I or IGF-II to receptor and for treating cancer in
PT   humans -
XX
PS   Disclosure; Figure 2A; 172pp; English.
XX
CC   This invention relates to a novel humanised, chimeric or human
CC   monoclonal antibody or its antigen binding portion that specifically
CC   binds to insulin-like growth factor I receptor (IGF-IR). The antibodies
CC   of the invention can act as an inhibitor of binding of IGF-I or IGF-II
CC   with IGF-IR and can inhibit in vivo tumour growth and IGF-IR tyrosine
CC   phosphorylation. The antibodies of the invention are useful for
CC   diagnosing the presence or location of an IGF-IR-expressing tumour in a
CC   subject. The antibody or its antigen-binding portion is also useful for
CC   treating cancer in a human. The method for this further involves an anti
CC   neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent.
CC   The antibodies may also be useful for increasing IGF-IR activity and
CC   thus restoring IGF-IR activity in a condition characterised by low
CC   IGF-IR levels e.g. neuropathy, or osteoporosis. An antibody of the
CC   invention is also useful for inducing apoptosis of specific cells in a
CC   patient, and to treat non-cancerous states or disease, e.g. acromegaly,
CC   gigantism, psoriasis and atherosclerosis. Fully human anti-IGF-IR
CC   antibodies minimise the immunogenic and allergic responses intrinsic to
CC   mouse or mouse-derivatised monoclonal antibodies and thus increase the
CC   efficacy and safety of the administered antibodies. The present sequence
CC   represents a DNA sequence encoding an anti-insulin-like growth
CC   factor I receptor antibody of the invention.                       .
XX
SQ   Sequence 376 BP; 87 A; 91 C; 110 G; 82 T; 6 other;

Query Match             68.4%;  Score 268.8;  DB 24;  Length 376;
Best Local Similarity   83.8%;  Pred. No. 4.1e-70;
Matches 310; Conservative    6; Mismatches  48;  Indels   6;  Gaps   1;

Qy      24 GGTGGGAGTCTGGGGGAGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTTCCTGTGTCAGC  83
           |||||:|||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db      12 GGTGGGAGTCTGGGGGAGGCCTTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGTGCAGC  71

Qy      84 CTCTGGATTCACCTTCAGTAGCTATAGCACATGCACTGGGTGCGCCAGGCTCCAGGGAAGGG  143
           ||||||||||:|||||||| |||||:|||||||||||||||||||||||||||||:||||||
Db      72 CCCTGGAATTCACCTTCAGTGACTACTATATGAGCTGGATCCGCCAGGCCCCAGGGAAGGG  131

Qy     144 GCTGGAGTGGGGTCTCATCCATTAGTAATAATAACTTACATATACTACGCAGACGCCAGT  203
           ||||||||| ||||| ||:|||||||:||:||||| ||:|:|||||||||||||||||||
Db     132 GCTGGAGTGGGTTTCATACATTAGTAGTAGTGGTAGTACCAAAKAACTACGCAGACTCTGT  191

Qy     204 GAAGGGCCGATTCACCATCTCCAGAGACAAACGCCAAGAACTCACTGTATCTGCAAATGAA  263
           ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     192 GAAGGGCCGATTCACCATCTCCAGGGACAACGCCAAGAACTCACTGTATCTGCAAATGAA  251

Qy     264 CAGCCTGAGAGCCGAGGACACACGGCTGTGTATTACTGTGCGAGAGATTCTAGATACAGTAA  323
           |||||||||||||||||||||||||| ||||||||||||||||||||| |||:||||||
Db     252 CAGCCTGAGAGCCGAGGACACGCGTATTACTGTGYGAGAGATGGAGTGGAAAACTAC  311

Qy     324 CAGCCTGAGAGCCGAGGACACACGGCTGTATTACTGTGGGCCAAGGGACCACGGTCAT  383
           ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db     252 TTTCCTCGAGCTTGGGTGGGACGGGGGTATGGACGGCTCTGGGGCCAAGGGACCACGGTCAC  311

Qy     324 CAGCCTGAGAGCCGAGGACACACGGCTGTATTACTGTGYGAGAGATGGAGTGGAAAACTAC  311

Qy     384 CGTCTCCTCA  393
           ||||||||||
Db     312 TTT----------TTACTACTTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCAC  365
```

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Db     366 CGTCTCCTCA 375

RESULT 12
AAD46294
ID   AAD46294 standard; DNA; 348 BP.
XX
AC   AAD46294;
XX
DT   27-DEC-2002  (first entry)
XX
DE   Human KDR (VEGFR-2) Fab heavy chain (VH) DNA from D2H2 clone.
XX
KW   Human; tumour; vascular endothelial growth factor receptor; metastasis;
KW   epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC;
KW   breast; VEGFR; heart; EGFR; therapy; invasiveness; heavy chain; gene;
KW   VH; ds.
XX
OS   Homo sapiens.
XX
FH   Key              Location/Qualifiers
FH
FT   CDS              1..348
FT                    /*tag= a
FT                    /product= "Human KDR (VEGFR-2) Fab heavy chain (VH)
FT                    protein"
FT                    /note= "CDS does not include start and stop codon"
FT                    /partial
XX
PN   WO200270008-A1.
XX
PD   12-SEP-2002.
XX
PF   04-MAR-2002; 2002WO-US067062.
XX
PR   02-MAR-2001; 2001US-0798689.
XX
PA   (IMCL-) IMCLONE SYSTEMS INC.
PA   (ROCK/) ROCKWELL P.
PA   (GOLD/) GOLDSTEIN N I.
XX
DR   WPI; 2002-691738/74.
DR   P-PSDB; AAE28873.
XX
PT   Inhibiting tumor growth in humans involves administering vascular
PT   endothelial growth factor receptor antagonists in combination with
PT   radiation, chemotherapeutic agents, or epidermal growth factor receptor
PT   antagonists -
XX
PS   Example 12; Page 126; 151pp; English.
XX
CC   The invention relates to a method of inhibiting tumour growth which
CC   involves administering vascular endothelial growth factor receptor
CC   (VEGFR) antagonists in combination with radiation, chemotherapeutic
CC   agent, or epidermal growth factor receptor (EGFR) antagonist. The method
CC   is useful for inhibiting tumour growth in a human, where the tumour (e.g.
CC   tumour of the breast, heart, lung, small intestine, colon, spleen, bone,
CC   kidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin,
CC   bone marrow, blood, thymus, uterus, testicles, cervix or liver) over
CC   expresses VEGFR. It is also useful for inhibiting growth of colon tumour
CC   or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR.
CC   It is preferably useful for treating subjects with both solid tumours,
CC   preferably high vascular tumours and non-solid tumours. The inhibition
CC   or reduction of tumour growth includes prevention or inhibition of the
CC   progression of tumour, including cancerous and non-cancerous tumours,
CC   where the progression of tumours includes the invasiveness, metastasis,
CC   recurrence and increase in size of the tumour. The present sequence is
CC   human KDR (VEGFR-2) Fab antibody heavy chain DNA.
XX
SQ   Sequence 348 BP; 82 A; 85 C; 105 G; 76 T; 0 other;

Query Match             68.2%;  Score 268;  DB 24;  Length 348;
Best Local Similarity   96.5%;  Pred. No. 7e-70;
Matches 274; Conservative    0; Mismatches  10;  Indels   0;  Gaps   0;
```

Qy   24 GGTGGAGTCTGGGGGAGGCCTGCTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   12 GGTGCAGTCTGGGGGAGGCCTGGTGCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 71

Qy   84 CTCTGGATTCACCTTCAGTAGTCTATAGCACTGGGGTCCGCCAGGCTCCAGGGAAGGG 143
         ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   72 CTCTGGATTCACCTTCAGTAGCTATAGCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGG 131

Qy   144 GCTGGAGTGGGTGTCATCCATTAGTAATAGTAATAATTACATAATACGCACACGGCAGT 203
         ||||||||||||||||||||||||||| |||||||| ||||| ||||||| |||||||
Db   132 GCTGGAGTGGGTGTCATCCATTAGTAGTAGTAGTTACATAGTAGTTACACGCAGACTCAGT 191

Qy   204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
         |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db   192 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 251

Qy   264 CAGCCTGAGAGCCGAGGACACGGGCTGTGTATTACTGTGCGAGAG 307
         |||||||||||||||||||||||||||||||||||||||||
Db   252 CAGCCTGAGAGCCGAGGACACGGGCTGTGTATTACTGTGCGAGAG 295

RESULT 13
ABT23329
ID   ABT23329 standard; DNA; 348 BP.
XX
AC   ABT23329;
XX
DT   01-MAY-2003 (first entry)
XX
DE   VEGF binding related DNA SEQ ID NO 82.
XX
KW   Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;
KW   leukaemia cell; vascular endothelial growth factor; tumour;
KW   bispecific antigen-binding protein; human; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200300214-A1.
XX
PD   09-JAN-2003.
XX
PF   26-JUN-2002; 2002WO-US20332.
XX
PR   26-JUN-2001; 2001US-301299P.
XX
PA   (IMCL-) IMCLONE SYSTEMS INC.
XX
PI   Zhu Z;
XX
DR   WPI; 2003-201468/19.
DR   P-PSDB; ABJ26765.
XX
PS   Disclosure; Page 73-74; 98pp; English.
XX
PT   New bispecific antibodies having antigen-binding sites specific for a
PT   first vascular endothelial growth factor (VEGF) receptor and for a
PT   second VEGF receptor, useful for inhibiting migration of leukemia
PT   cells, or for treating tumors -
XX
CC   The invention relates to a novel antibody having a first antigen binding
CC   site specific for a first vascular endothelial growth factor (VEGF)
CC   receptor and a second antigen-binding site specific for a second VEGF
CC   receptor. The bispecific antigen-binding proteins block activation of the
CC   VEGF receptor and are useful for reducing or inhibiting VEGF-induced
CC   cellular functions such as mitogenesis of vascular endothelial cells
CC   and migration of leukaemia cells. The antibodies are useful for treating
CC   tumours and for in vivo or in vitro for investigative and diagnostic
CC   methods. This polynucleotide sequence represents a human DNA sequence
CC   relating to the bispecific antibodies that bind to the VEGF receptors of
CC   the invention.
XX
SQ   Sequence 348 BP; 82 A; 85 C; 105 G; 76 T; 0 other;

Query Match   68.2%;   Score 268;   DB 25;   Length 348;
Best Local Similarity   96.5%;   Pred. No. 7e-70;
Matches 274;   Conservative 0;   Mismatches 10;   Indels 0;   Gaps 0;

Qy   24 GGTGGAGTCTGGGGGAGGCCTGCTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
         |||| |||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   12 GGTGCAGTCTGGGGGAGGCCTGGTGCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 71

Qy   84 CTCTGGATTCACCTTCAGTAGCTATAGCACTGGGGTCCGCCAGGCTCCAGGGAAGGG 143
         |||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||
Db   72 CTCTGGATTCACCTTCAGTAGCTATAGCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGG 131

Qy   144 GCTGGAGTGGGTGTCATCCATTAGTAATAGTAATAATTACATAATACGCACACGGCAGT 203
         |||||||||||||||||||||||||||| |||||| ||||| ||||||| |||||||
Db   132 GCTGGAGTGGGTGTCATCCATTAGTAGTAGTAGTTACATAGTAGTTACACGCAGACTCAGT 191

Qy   204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
         ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   192 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 251

Qy   264 CAGCCTGAGAGCCGAGGACACGGGCTGTGTATTACTGTGCGAGAG 307
         |||||||||||||||||||||||||||||||||||||||||||||
Db   252 CAGCCTGAGAGCCGAGGACACGGGCTGTGTATTACTGTGCGAGAG 295

RESULT 14
AAH41153
ID   AAH41153 standard; DNA; 458 BP.
XX
AC   AAH41153;
XX
DT   22-AUG-2001 (first entry)
XX
DE   Human coding sequence SEQ ID 3.
XX
KW   Human; antiarthritic; cardiant; monoclonal antibody; keloid; arthritis;
KW   Tumour Growth Factor-beta II receptor; TGF-beta II receptor; atopy;
KW   signal transduction inhibition; tissue fibrosis; atherosclerosis; ds.
XX
OS   Homo sapiens.
XX
PN   WO200136642-A1.
XX
PD   25-MAY-2001.
XX
PF   17-NOV-2000; 2000WO-JP08129.
XX
PR   18-NOV-1999;   99JP-0328681.
PR   08-NOV-2000; 2000JP-0340216.
XX
PA   (NISB) JAPAN TOBACCO INC.
XX
PI   Sakamoto S; Kamada M;
XX
DR   WPI; 2001-3438225/36.
DR   P-PSDB; AAB99111.
XX
PS   Example 12; Page 94-95; 118pp; Japanese.
XX
PT   Human monoclonal antibodies recognizing human TGF-beta II receptor,
PT   useful for treating TGF-beta associated diseases such as tissue
PT   fibrosis -
XX
CC   The present invention relates to novel human monoclonal antibodies. The
CC   antibodies can bind to human Tumour Growth Factor-beta (TGF-beta) II
CC   receptor, resulting in the inhibition of the signal transduction of human
CC   TGF-beta into cells. The antibodies can be used for the prevention and
CC   treatment of diseases associated with the production of TGF-beta, such as
CC   tissue fibrosis in the lung, liver, skin, kidney or other tissues,
CC   atherosclerosis, atopy, keloid and arthritis. The present sequence was
CC   used in the present invention.
XX

SQ   Sequence 458 BP; 92 A; 121 C; 139 G; 106 T; 0 other;

Query Match   68.2%; Score 268; DB 22; Length 458;
Best Local Similarity 96.5%; Pred. No.7.7e-70;
Matches 274; Conservative   0; Mismatches 10; Indels   0; Gaps   0;

Qy   24 GGTGGAGTCTGGGGGGGGAGGCCTGGTCAAGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   69 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGC 128

Qy   84 CTCTGGATTCACCTTCAGTAGCTATATAGCAATGCACTGGGTCCGCCAGGGTCCAGGGAAGGG 143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   129 CTCTGGATTCACCTTCAGTAGCTTTAGCATGAACTGGGTCCGCCAGGCTCCAGGGAAGGG 188

Qy   144 GCTGGAGTGGGTCTCATCCATTTAGTAAATAGTAATTACTTTACATATATATCACGGCACCAGCGCAGT 203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   189 GCTGGAGTGGGTCTCATCCATTTAGTAGTTACATTAACTACACAGACTCAGT 248

Qy   204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAAATGAA 263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   249 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAAATGAA 308

Qy   264 CAGCCTGAGAGCCGAGCACACGGCGTGTGTTACTACTGTGCGAGAG 307
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   309 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG 352

RESULT 15
ABS62704
ID   ABS62704 standard; DNA; 376 BP.
AC   ABS62704;
XX
DT   24-OCT-2002 (first entry)
XX
DE   Anti-IGF-IR antibody (4.9.2) variable region heavy chain DNA.
XX
KW   Insulin-like growth factor I receptor; antibody; human; ds; gene;
KW   cytostatic; osteopathic; antiatherosclerotic; antipsoriatic;
KW   IGF-IR; tumour; anti-neoplastic; anti-tumour; anti-angiogenic;
KW   neuropathy; osteoporosis; acromegaly; gigantism; psoriasis;
KW   atherosclerosis.
XX
OS   Homo sapiens.
XX
PN   WO200253596-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-US51113.
XX
PR   05-JAN-2001; 2001US-259927P.
XX
PA   (PFIZ) PFIZER INC.
PA   (ABGE-) ABGENIX INC.
XX
PI   Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;
XX
DR   WPI; 2002-575410/61.
DR   P-PSDB; ABG77142.
XX
PT   Novel humanised, chimeric monoclonal antibody that specifically binds
PT   to insulin-like growth factor I (IGF-1) receptor useful for inhibiting
PT   binding of IGF-I or IGF-II to receptor and for treating cancer in
PT   humans -
XX
PS   Disclosure; Figure 2C; 172pp; English.
XX
CC   This invention relates to a novel humanised, chimeric or human
CC   monoclonal antibody or its antigen binding portion that specifically
CC   binds to insulin-like growth factor I receptor (IGF-IR). The antibodies
CC   of the invention can act as an inhibitor of binding of IGF-I or IGF-II
CC   with IGF-IR and can inhibit in vivo tumour growth and IGF-IR tyrosine

CC   phosphorylation. The antibodies of the invention are useful for
CC   diagnosing the presence or location of an IGF-IR-expressing tumour in a
CC   subject. The antibody or its antigen-binding portion is also useful for
CC   treating cancer in a human. The method for this further involves an anti
CC   neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent.
CC   The antibodies may also be useful for increasing IGF-IR activity and
CC   thus restoring IGF-IR activity in a condition characterised by low
CC   IGF-IR levels e.g. neuropathy or osteoporosis. An antibody of the
CC   invention is also useful for inducing apoptosis of specific cells in a
CC   patient, and to treat non-cancerous states of disease, e.g. acromegaly,
CC   gigantism, psoriasis and atherosclerosis. Fully human anti-IGF-IR
CC   antibodies minimise the immunogenic and allergic responses intrinsic to
CC   mouse or mouse-derivatised monoclonal antibodies and thus increase the
CC   efficacy and safety of the administered antibodies. The present sequence
CC   represents a DNA sequence encoding an anti-insulin-like growth
CC   factor I receptor antibody of the invention.
XX
SQ   Sequence 376 BP; 95 C; 117 G; 84 T; 0 other;

Query Match   66.6%; Score 261.6; DB 24; Length 376;
Best Local Similarity 83.8%; Pred. No. 5.8e-68;
Matches 310; Conservative   0; Mismatches 54; Indels   6; Gaps   1;

Qy   24 GGTGGAGTCTGGGGGGGGAGGCCTGGTCAAGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
          |||||||||||||| |||||||||||||||| ||||||||||||||||||||||||||||||||
Db   12 GTTGGAGTCTGGGGGAGGCCTTGGGTACAGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGC 71

Qy   84 CTCTGGATTCACCTTCAGTAGCTATAGCAATGCACTGGGTCCGCCAGGGTCCAGGGAAGGG 143
          ||||||||||||||||||||| |||||||||||| |||||||||||||||||||||||||
Db   72 CTCTGGATTCACCTTAGCAGCTATTAGCCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGG 131

Qy   144 GCTGGAGTGGGTCTCATCCATTTAGTAATAGTAATTACTTTACATATATATCACGGCACCAGCGCAGT 203
          |||||||||||| |||| |||||| |||||||| |||| ||||||||||| ||||||
Db   132 GCTGGAGTGGGTCTCAGCTATTAGTAGTAATAGTTACATTAATACTTACAGCGACGACTCGT 191

Qy   204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAAATGAA 263
          ||||||||||| ||||| |||||||| |||||||| ||||||||| |||||||||||
Db   192 GAAGGGCCGGTTCACCATCTCCAGAGACAACACCAAGCTGGTGTATCTGCAAAATGAA 251

Qy   264 CAGCCTGAGAGCCGAGCACACGGCGTGTGTTACTACTGTGCGAGAG 307
          ||||||||| | ||| |||| ||| | |||||||||||||||
Db   252 CAGCCTGAGAGCCGAGGACACGGCGTATATTACTGTGCGAAAGATCTGGGCTACGGTGA 311

Qy   324 TTTCCTCCGTTGGGTTCGGAGCCGACGGTATGGACGTCTGGGGCCCAAGGGACCACGGTCAT 383
          |||||||||||||||| ||| ||| || |||| || ||||||||||||||||||||
Db   312 CTT------TTACTACTACTACGGTATGGACGTCTGGGGCCCAAGGGACCACGGTCAC 365

Qy   384 CGTCTCCTCA 393
          ||||||||||
Db   366 CGTCTCCTCA 375

RESULT 16
AAX77236
ID   AAX77236 standard; DNA; 381 BP.
AC   AAX77236;
XX
DT   04-AUG-1999 (first entry)
XX
DE   Human D4.5 heavy chain variable region encoding DNA.
XX
KW   Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
KW   autoimmune disease; scFv-antibody; single-chain Fv; ss.
XX
OS   Homo sapiens.
XX
PN   WO9925818-A1.
XX
PD   27-MAY-1999.
XX
PF   16-NOV-1998; 98WO-EP07313.
XX

Left record

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RESULT 17
AAV68537
ID   AAV68537 standard; DNA; 414 BP.
XX
AC   AAV68537;
XX
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```
PR   17-NOV-1997; 97EP-0120096.
XX
PA   (KUFE/) KUFER P.
XX
PI   Borschert K, Kufer P, Lutterbuese R, Raum T, Zettl F;
XX
DR   WPI; 1999-338004/28.
DR   P-PSDB; AAY17954.
XX
PT   Phage display system for identification of binding site domains
PT   retaining capacity to bind an epitope
XX
PS   Disclosure; Fig 3.1; 152pp; English.
XX
CC   The invention relates to a method of identifying binding site domains
CC   (BSD) that retain the capacity of binding to a predetermined epitope when
CC   positioned C-terminal of at least one further domain in a recombinant bi-
CC   or multivalent polypeptide. The method comprises (a) testing a panel of
CC   BSD displayed on the surface of a biological display system as part of a
CC   fusion protein for binding to a predetermined epitope, where the fusion
CC   protein comprises an additional domain positioned N-terminal of the BSD
CC   and an amino acid sequence that mediates anchoring of the fusion protein
CC   to the surface of the display system; and (b) identifying a BSD that
CC   binds to the predetermined epitope. The method is useful to identify bi-
CC   or multivalent polypeptides that comprise antibody binding sites capable
CC   of efficiently binding to the corresponding antigen. The polypeptides or
CC   antibodies identified by the method are useful therapeutically and
CC   diagnostically, for e.g. cancer and autoimmune diseases. ScFv-antibody
CC   fragments that bind independently of their position within bifunctional
CC   single-chain fusion proteins can be isolated from combinatorial antibody
CC   libraries using the new in vitro method.
XX
SQ   Sequence 381 BP; 87 A; 93 C; 120 G; 81 T; 0 other;
```

```
Query Match            66.5%;  Score 261.2;  DB 20;  Length 381;
Best Local Similarity  81.6%;
Matches 302;  Conservative 0;  Pred. No. 7.6e-68;  Mismatches 68;  Indels 0;  Gaps 0;
```

```
Qy    24  GGTGGGAGTCTGGGGGGAGGGCTGGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCACC    83
          | |||||||||||||||||||  |||||| ||  ||| |||||||||||||||||||||||||
Db    12  GCTCGAGTCTGGGGGGAGGCGTGGGTCCACGCTGGGAGGCGTGGTCCCTGAGACTCTCCTGTGCACC  71

Qy    84  CTCTGGATTCACCTTCAGTAGCTATAGCATGGCACTGGGTCCGCCAGGGTCCAGGGAAGGG     143
          |||||||||||||||||||||||||||| |||||||||||||||||| ||||||  |||||
Db    72  CTCTGGATTCACCTTCAGTAGCTATAGCACTGGGTCCGCCAGGCTCCAGGCAAGGG         131

Qy   144  GCTGGAGTGGGTCTCATCCATTAGTAGTAATACTTACATTATAATACTACGCAGACGCAGT    203
          ||||||||||| |||   ||| ||| |||  |||||||||||||||||||||||||||||||
Db   132  GCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAAATACTACTATACGCAGACTCCGT    191

Qy   204  GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA     263
          ||||| |||||||||||||||||||||||||||||||||||||||| |||| ||||||||
Db   192  GAAGGGCCGATTCACCATCTCCAGAGACAACGCCTGTATCTGCAAATGAA               251

Qy   264  CAGCCTGAGAGCCGAGGACACACGGCTGTGTACTACTGTGCGAGAGATTCTAGATACAGTAA   323
          |||||||||||||||||||||||| ||||||||||| | |||||| |||||||||||||||
Db   252  CAGCCTGAGAGCTGAGGACACGGCGCTGTGTATTACTGTGCGAAAGATATGGGGTGGGCAG    311

Qy   324  TTTCCTCCGTTGGGTTCGGAGGCTCGGGGACGGTATGGCACGTCTCGGGGCAGCCAGGGTCAT   383
          |  |||| ||||||||||||||||||||||||||| |||||||||||||||||||||
Db   312  TGGCTGGAGACCCTACTACTACGGTATGGACGTCTCGGGGCCAAGGGACCACGGTCAC      371

Qy   384  CGTCTCCTCA    393
          ||||||||||
Db   372  CGTCTCCTCA    381
```

Right record

```
DT   16-FEB-1999  (first entry)
XX
DE   Nucleotide sequence of human D4.5 heavy chain variable region.
XX
KW   Human; D4.5 heavy chain variable region; receptor; antigen;
KW   tumour; auto-immune disease; graft rejection; allergy;
KW   inflammatory disease; endocrine disease; degenerative disease; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FH
FT   CDS             1..414
FT                   /*tag= a
FT                   /product= "human D4.5 heavy chain variable
FT                   region"
XX
PS   Claim 9; Fig 7; 84pp; English.
XX
PT   Production of anti-human antigen receptors - by selecting a
PT   combination of functionally rearranged VH and VL immunoglobulin
PT   chains expressed from a recombinant vector
XX
DR   WPI; 1998-594564/50.
DR   P-PSDB; AAW80815.
XX
PI   Kufer P, Raum T;
XX
PA   (KUFE/) KUFER P.
PA   (RAUM/) RAUM T.
XX
PR   14-APR-1997; 97EP-0106109.
PF   14-APR-1998; 98WO-EP02180.
PD   22-OCT-1998.
PN   WO9846645-A2.
XX
CC   This is the nucleotide sequence of the human D4.5 heavy chain
CC   variable region, used in the method of the invention, for providing
CC   receptors that can be used for targeting antigens in humans without
CC   being immunogenic themselves. Such receptors can be used for treating
CC   diseases such as tumours or auto-immune diseases, graft rejection
CC   after transplantation, infectious diseases by targeting cellular
CC   receptors as well as allergic, inflammatory, endocrine and
CC   degenerative diseases by targeting key molecules involved in the
CC   pathological process.
XX
SQ   Sequence 414 BP; 93 A; 106 C; 127 G; 88 T; 0 other;
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Query Match            66.5%;  Score 261.2;  DB 19;  Length 414;
Best Local Similarity  81.6%;
Matches 302;  Conservative 0;  Pred. No. 7.8e-68;  Mismatches 68;  Indels 0;  Gaps 0;
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Qy    24  GGTGGGAGTCTGGGGGGAGGGCTGGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCACC    83
          | |||||||||||||||||||  |||||| ||  ||| |||||||||||||||||||||||||
Db    12  GCTCGAGTCTGGGGGGAGGCGTGGGTCCACGCTGGGAGGCGTGGTCCCTGAGACTCTCCTGTGCACC  71

Qy    84  CTCTGGATTCACCTTCAGTAGCTATAGCATGGCACTGGGTCCGCCAGGGTCCAGGGAAGGG     143
          |||||||||||||||||||||||||||| |||||||||||||||||| ||||||  |||||
Db    72  CTCTGGATTCACCTTCAGTAGCTATAGCACTGGGTCCGCCAGGCTCCAGGCAAGGG         131

Qy   144  GCTGGAGTGGGTCTCATCCATTAGTAGTAATACTTACATTATAATACTACGCAGACGCAGT    203
          ||||||||||| |||   ||| ||| |||  |||||||||||||||||||||||||||||||
Db   132  GCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAAATACTACTATACGCAGACTCCGT    191

Qy   204  GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA     263
          ||||| |||||||||||||||||||||||||||||||||||||||| |||| ||||||||
Db   192  GAAGGGCCGATTCACCATCTCCAGAGACAACGCCTGTATCTGCAAATGAA               251

Qy   264  CAGCCTGAGAGCCGAGGACACACGGCTGTGTACTACTGTGCGAGAGATTCTAGATACAGTAA   323
          |||||||||||||||||||||||| ||||||||||| | |||||| |||||||||||||||
Db   252  CAGCCTGAGAGCTGAGGACACGGCGCTGTGTATTACTGTGCGAAAGATATGGGGTGGGCAG    311
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Left column

```
Qy   324 TTTCCTCCGTTGGGTTCGGACGGACGGTATGGACGTCTGGGGGCCAAGGGACCACGGTCT 383
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   312 TGGCTGGAAGACCCTACTACTACTACGTATGGACGTCTGGGGCCAAGGGACCACGGTCAC 371

Qy   384 CGTCTCCTCA 393
         ||||||||||
Db   372 CGTCTCCTCA 381
```

RESULT 18

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AA220407
ID   AA220407 standard; cDNA; 519 BP.
XX
AC   AA220407;
XX
DT   19-NOV-1999  (first entry)
XX
DE   IgG antibody 2.1.1 heavy chain coding sequence.
XX
KW   Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;
KW   activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW   organ transplant rejection disease; lymphoma; pancreatic disease;
KW   autoimmune disease; inflammatory disease; arthritis; binding site; ss.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
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FT   CDS            1..519
FT                  /tag= a
FT                  /note= "no stop codon given"
XX
PN   WO9945031-A2.
XX
PD   10-SEP-1999.
XX
PF   03-MAR-1999.
XX
PR   03-MAR-1998;  99WO-US04583.
PR   03-FEB-1999;  99US-0244253.
PR                 98US-0034607.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Davis CG,  Blacher RW,  Corvalan JR,  Culwell AR,  Green LL,  Hales J;
PI   Havrilla N,  Ivanov VE,  Lipani JA,  Liu Q,  Weber RF,  Yang X;
XX
DR   WPI; 1999-540816/45.
DR   P-PSDB; AAY34306.
XX
PT   New monoclonal antibody, used for treating e.g. graft versus host
PT   disease, cancers, autoimmune diseases and inflammatory diseases -
XX
PS   Disclosure; Fig 31; 245pp; English.
XX
CC   This sequence encodes the heavy chain of an antibody of the
CC   invention. The antibody is a monoclonal antibody (MAb) with an isotype
CC   that fixes complement and a variable region that binds to the epitope on
CC   CD147 bound by the IgM MAb ABX-CBL, providing that the antibody is not
CC   CBll. The MAb can selectively kill activated T-cells, activated B-cells
CC   or resting or activated monocytes. The products and methods can be used
CC   for treating diseases involving activated T-cells or B-cells or
CC   monocytes, e.g. graft versus host disease (GVHD), organ transplant
CC   rejection diseases (e.g. renal transplant, ocular transplant), cancers
CC   (e.g. cancers of the blood (e.g. leukaemia's and lymphomas) and
CC   pancreatic)/autoimmune diseases (e.g. lupus), and inflammatory diseases
CC   (e.g. arthritis).
XX
SQ   Sequence 519 BP; 109 A; 155 C; 151 G; 104 T; 0 other;

Query Match         66.3%;  Score 260.6; DB 20;  Length 519;
Best Local Similarity   93.5%;
Matches 272;   Conservative   0; Mismatches   19;   Indels   0;  Gaps   0;
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Right column

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Qy    34 GGGGGAGGCGTTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTC 93
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Db     1 GGGGAAGGCGTTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTC 60

Qy    94 ACCTTCAGTAGCTATAGCATCCACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGG 153
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 ACCTTCAGTAGCTATAGCATGCATTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGG 120

Qy   154 GTCTCATCCATTAGTAATGGTAATACTTACATATATTACGCAGACTCAGTGAAGGGCCGA 213
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GTCTCATCCATTAGTAGTAGTAGTACATATATTACGCAGACTCAGTGAAGGGCCGA 180

Qy   214 TTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAACAGCCTGAGA 273
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAACAGCCTGAGA 240

Qy   274 GCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATTCTAGATACAGTAAT 324
         |||||||||||||||||||||||||||||||||||||||||| |||
Db   241 GCCGAGGACACGGCTGTGTATTACTGTGCGAGGATTAGCAGTGGCTGGTAT 291

RESULT 19
AA250587
ID   AA250587 standard; DNA; 1630 BP.
XX
AC   AA250587;
XX
DT   23-MAY-2000  (first entry)
XX
DE   HD70scFv-CH1-GM-CSF chain encoding DNA.
XX
KW   HD70; single-chain variable fragment; scFv; 17-1A antigen; human;
KW   EpCAM; epithelial cell adhesion molecule; inflammatory cytokine; GM-CSF;
KW   granulocyte/macrophage colony stimulating factor; heterodimeric;
KW   CH1-domain; multifunctional compound; heavy chain constant domain;
KW   immunoglobulin; cytostatic; immunostimulatory; antileukaemia; diagnosis;
KW   antiproliferative; prevention; treatment; malignant; haematopoietic cell;
KW   lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma; ds.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
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FT                  /tag= a
FT                  /product= "HD70scFv-CH1-GM-CSF chain"
FT   misc_feature   96..842
FT                  /tag= b
FT                  /label= HD70_scFv
XX
PN   WO200006605-A2.
XX
PD   10-FEB-2000.
XX
PF   28-JUL-1999;  99WO-EP05416.
XX
PR   28-JUL-1998;  98EP-0114082.
XX
PA   (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.
XX
PI   Kufer P,  Dreier T,  Baeuerle PA,  Borschert K,  Zettl F;
XX
DR   WPI; 2000-192265/17.
DR   P-PSDB; AAY44994.
XX
PT   New multifunctional compounds useful for preventing and/or treating
PT   malignant cell growth and for detection and diagnosis -
XX
PS   Claim 8; Fig 55A; 166pp; English.
XX
CC   The patent discloses heterominibodies which are multifunctional compounds
CC   produceable in a mammalian host cell as a secretable and fully functional
CC   heterodimer of two polypeptide chains, where one of the polypeptide
CC   chains comprises, a CH1-domain (constant domain of an immunoglobulin
```

Left column:

```
CC   heavy chain) and the other chain comprises CL-domain (constant domain of
CC   an immunoglobulin light chain). The polypeptide chains further comprise,
CC   fused to the constant domains at least two (poly)peptides having
CC   different (poly)peptides lack an intrinsic affinity for one another and
CC   different receptor or ligand functions, where further at least two of the
CC   are linked via the constant domains. The heterominibodies have
CC   cytostatic, immunostimulatory, antileukaemia and antiproliferative
CC   activities. These compounds can be used for diagnosing, preventing and
CC   treating malignant cell growth related to malignancies of haematopoietic
CC   cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,
CC   melanomas and sarcomas.
CC   The present sequence is a DNA encoding left chain of a heterominibody
CC   comprising HD70 single-chain Fv (scFv) fragment N-terminally linked to
CC   human CH1 domain which bears at its C-terminus the human inflammatory
CC   cytokine granulocyte/macrophage colony stimulating factor (GM-CSF), plus
CC   a hexahistidine sequence for ease of purification. HD70 scFv
CC   specifically recognises the human epithelial cell adhesion molecule
CC   (EpCAM) also called 17-1A antigen.
XX
SQ   Sequence 1630 BP; 376 A; 484 C; 437 G; 333 T; 0 other;
```

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Query Match      66.2%;  Score 260.2;  DB 21;  Length 1630;
Best Local Similarity   81.6%;  Pred. No. 2.4e-67;
Matches 301;  Conservative   0;  Mismatches  68;  Indels   0;  Gaps   0;

Qy   24 GGTGGAGTCTGGGGGAGGCGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
         | |||||||||||||||||||| |||||||||||||||| |||||| ||||| |||||||
Db  473 GCTGGAGTCTGGGGGAGGCGTGGTCCCAGCCTGGGGAGGTCCCTGAGACTCTCCTGTGCAGC 532

Qy   84 CTCTGGATTCACCTTCAGTAGTAGCTATAGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGG 143
         |||||||||||||||||||||||||| ||||||||||
Db  533 CTCTGGATTCACCTTCAGTAGTAGCTATAGCCATGCACTGGGTCCGCCAGGCTCCAGGGAAGG 592

Qy  144 GCTGGAGTCGGGGTGGGCAGTTATATCATTAGTAATAGTAATACTTACATATATCACGGCAGT 203
         |||||||| |||||||||||||||||||| |||||||||||||||||||||||||| ||
Db  593 GCTGGAGTGGGGGTGGGCAGTTATATCATGGAAGTAATAAATACTTACACGGCAGT 652

Qy  204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACGTATCTGCAAATGAA 263
         ||||||||||||||||| |||||||||||  | |||||||||||| |||||||||||||
Db  653 GAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAA 712

Qy  264 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCCAAAGATATGGGTGGGGCAG 323
         |||||||||||| |||||||| ||||| |||||||||||| |||||| ||||
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Qy  324 TTTCCTCCGTTGGGGTTCGGAGCGGACGGATGGAACGTCTGGGCCAAAGGACCACGGGTCAT 383
         |      |||||||| |||||||||||  | ||||| |||||||| |||||||| |||||
Db  773 TGGCTGGAGACCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCAC 832

Qy  384 CGTCTCCTC 392
         |||||||||
Db  833 CGTCTCCTC 841
```

```
RESULT 20
AA250588
ID   AA250588 standard; DNA; 1630 BP.
XX
AC   AA250588;
XX
DT   23-MAY-2000  (first entry)
XX
DE   HD70scFv-Ck-interleukin 2 encoding DNA.
XX
KW   HD70; single-chain variable fragment; scFv; 17-1A antigen; human;
KW   EpCAM; epithelial cell adhesion molecule; inflammatory cytokine;
KW   IL-2; interleukin-2; Ck domain; kappa light chain constant domain;
KW   heterominibody; multifunctional compound; immunoglobulin;
KW   cytostatic; immunostimulatory; antileukaemia; diagnosis; prevention;
KW   antiproliferative; treatment; malignant; haematopoietic cell; lymphoma;
KW   leukaemia; solid tumour; carcinoma; melanoma; sarcoma; ds.
XX
OS   Homo sapiens.
```

Right column:

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FT                   /product= "HD70scFv-Ck-IL-2 chain"
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FT                   /*tag= b
FT   misc_feature    /label= HD70_scFv
XX
PN   WO200006605-A2.
XX
PD   10-FEB-2000.
XX
PF   28-JUL-1999;  99WO-EP05416.
XX
PR   28-JUL-1998;  98EP-0114082.
XX
PA   (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.
XX
PI   Kufer P, Dreier T, Baeuerle PA, Borschert K, Zettl F;
XX
DR   WPI; 2000-195265/17.
DR   P-PSDB; AAY44995.
XX
PT   New multifunctional compounds useful for preventing and/or treating
PT   malignant cell growth and for detection and diagnosis -
XX
PS   Claim 8; Fig 55B; 166pp; English.
XX
CC   The patent discloses heterominibodies which are multifunctional compounds
CC   produceable in a mammalian host cell as a secretable and fully functional
CC   heterodimer of two polypeptide chains, where one of the polypeptide
CC   chains comprises, a CH1-domain (constant domain of an immunoglobulin
CC   heavy chain) and the other chain comprises CL-domain (constant domain of
CC   an immunoglobulin light chain). The polypeptide chains further comprise,
CC   fused to the constant domains at least two (poly)peptides having
CC   different receptor or ligand functions, where further at least two of the
CC   different (poly)peptides lack an intrinsic affinity for one another and
CC   are linked via the constant domains. The heterominibodies have
CC   cytostatic, immunostimulatory, antileukaemia and antiproliferative
CC   activities. These compounds can be used for diagnosing, preventing and
CC   treating malignant cell growth related to malignancies of haematopoietic
CC   cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,
CC   melanomas and sarcomas.
CC   The present sequence is a DNA encoding right chain of a heterominibody
CC   comprising HD70 single-chain Fv (scFv) fragment N-terminally linked to
CC   human Ck domain (constant domain of immunoglobulin-kappa light chain)
CC   which bears at its C-terminus the human inflammatory cytokine
CC   interleukin-2 (IL-2). HD70 scFv specifically recognises the human
CC   epithelial cell adhesion molecule (EpCAM) also called 17-1A antigen.
XX
SQ   Sequence 1630 BP; 445 A; 410 C; 367 G; 367 T; 0 other;
```

```
Query Match      66.2%;  Score 260.2;  DB 21;  Length 1630;
Best Local Similarity   81.6%;  Pred. No. 2.4e-67;
Matches 301;  Conservative   0;  Mismatches  68;  Indels   0;  Gaps   0;

Qy   24 GGTGGAGTCTGGGGGAGGCGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
         | |||||||||||||||||||| |||||||||||||||| |||||| ||||| |||||||
Db  473 GCTGGAGTCTGGGGGAGGCGTGGTCCCAGCCTGGGGAGGTCCCTGAGACTCTCCTGTGCAGC 532

Qy   84 CTCTGGATTCACCTTCAGTAGTAGCTATAGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGG 143
         |||||||||||||||||||||||||| ||||||||||
Db  533 CTCTGGATTCACCTTCAGTAGTAGCTATAGCCATGCAGT 592

Qy  144 GCTGGAGTCGGGGTGGGCAGTTATATCATTAGTAATAGTAATACTTACATATATCACGGCAGT 203
         |||||||| |||||||||||||||||||| ||||||||||||||
Db  593 GCTGGAGTGGGGGTGGGCAGTTATATCATGGAAGTAATAAATACTTACAGGCAGT 652

Qy  204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACGTATCTGCAAATGAA 263
         ||||||||||||||||| |||||||||||  | ||||||||||||||||||||||||||
Db  653 GAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAA 712
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```
Qy    264  CAGCCTGAGAGCCGAGCACACGGCCTGTGTACTACTGTGCCGAGAGATTCTAGATTACAGTAA  323
           |||||||||||| ||| |||||||||||||| |||||||| |  |     |  |
Db    713  CAGCCTGAGAGCTGAGGACACGGCCTGTGTATTACTGTGCGAAAGATTATGGGGTGGGGCCAG  772

Qy    324  TTTCCTCCGTTGGGTTCGGGAGCCAAGGGACCACGGTCAT  383
           |   |       |  | |||||||||||||||||||||||
Db    773  TGGCTGGAGACCCTACTACTACTACGGTATGGACGGTCTCGGGGGCCAAGGGACCACGGTCAC  832

Qy    384  CGTCTCCTC  392
           |||||||||
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Job time : 271 secs

OM nucleic - nucleic search, using sw model

Run on: September 24, 2003, 02:42:43 ; Search time 2280 Seconds
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                                             4189.324 Million cell updates/sec

                        GenCore version 5.1.6
                        Copyright (c) 1993 - 2003 Compugen Ltd.

Title: US-09-848-798A-97
Perfect score: 393
Sequence: 1 gaggtgcagctgctcgagtc.........ccacgtcatcgtccctca 393

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 60 summaries

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SUMMARIES

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11	268.2	68.2	908	10	BG686881	BG686881 602650867
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25	255	64.9	988	13	BQ712092	BQ712092 AGENCOURT
26	254	64.6	445	10	AW408316	AW408316 UI-HF-BK0
27	254	64.6	876	10	BG758406	BG758406 602712604 UI-HF-BK0
28	253.6	64.5	618	12	BM713479	BM713479 UI-E-EJ0-
29	252	64.1	326	13	BE150045	BE150045 QVO-HT036
30	251.2	63.9	530	12	BM819424	BM819424 K-EST0087
31	250.8	63.8	669	10	BG686716	BG686716 602650678
32	250.8	63.8	471	13	BM848820	BM848820 K-EST0128
33	250.6	63.8	556	12	BM820006	BM820006 K-EST0088
34	250.6	63.8	567	12	BM820534	BM820534 K-EST0089
35	250.6	63.8	640	12	BM819504	BM819504 K-EST0087
36	250.6	63.8	406	9	AW408304	AW408304 UI-HF-BK0
37	250.6	63.8	801	13	BX399298	BX399298
38	250.4	63.7	792	10	BF129047	BF129047 K-EST0087
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41	249	63.4	932	13	BQ711605	BQ711605
42	248.4	63.2	390	10	AW408285	AW408285 UI-HF-BK0
43	248.4	63.2	440	9	AW408304	AW408304 UI-HF-BK0
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45	247.4	63.0	705	10	BG758682	BG758682 602712929
46	247.2	62.9	942	13	BQ710859	BQ710859 AGENCOURT
47	247.2	62.9	957	13	BQ894558	BQ894558 AGENCOURT
48	246.6	62.7	979	13	BQ708029	BQ708029 AGENCOURT
49	246.6	62.7	378	9	AA740786	AA740786 ob32e11.s
50	246.4	62.7	859	13	BX368110	BX368110
51	246.2	62.6	860	13	BQ705956	BQ705956 AGENCOURT
52	246	62.6	456	9	AW403059	AW403059 UI-HF-BK0
53	245.4	62.4	902	12	BM007556	BM007556
54	245	62.3	481	14	CA397706	CA397706 cs94f03.y
55	244.8	62.3	894	13	BQ708235	BQ708235 AGENCOURT
56	244.6	62.2	436	12	BM820963	BM820963 K-EST0089
57	244.4	62.2	516	9	AW401728	AW401728 UI-HF-BK0
58	244.4	62.2	973	10	BG397895	BG397895 602439405
59	244.4	62.2	984	13	BQ709776	BQ709776 AGENCOURT
60	244	62.1	964	13	BQ708077	BQ708077 AGENCOURT

ALIGNMENTS

RESULT 1
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LOCUS   BG757947   740 bp   mRNA   linear   EST 15-MAY-2001
DEFINITION   602714983F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4854932 5',
                mRNA sequence.
ACCESSION   BG757947
VERSION   BG757947.1 GI:14068600
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE    1 (bases 1 to 740)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM1703 row: f  column: 21
             High quality sequence stop: 736.
FEATURES             Location/Qualifiers
     source          1..740
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4854932"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_48"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT     166 a    203 c    206 g    165 t
ORIGIN

Query Match          77.0%;    Score 302.8;   DB 10;    Length 740;
Best Local Similarity 88.6%;   Pred. No. 9.4e-73;
Matches 328; Conservative   0; Mismatches  42;  Indels   0;  Gaps   0;

Qy     24 GGTGGGAGTCTGGGGGGAGGGCCTGGTCCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC  83
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Db     92 GGTGGGAGTCTGGGGGAGGGCTTGGTCACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC  151

Qy     84 CTCTGGATTCACCTTCACTTCAGTAGCTATATAGCAATGCACTCAGGGTCCGGGGTCCAGGGAAGG  143
          |-||||||||||||||||||||||-|||| |||| || |||||||||||||||||||||||||||
Db    152 CTCTGGATTCACCTTCAGTAGCTATAGCAATGAACTCGGGGTCCGCGCCAGGCTTCCAGGGAAGG  211

Qy     24 GCTGGAGTGGGTCTCATCCATTAGTAAATAGTAATATTACATAATAACTACGCAACGGCAGT  203
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Db    212 GCTGGAGTGGGTTTCATACATTAGTAGTAGTACCATATAACTACGCAGACTCTGT  271

Qy    204 GAAGGGCCGATTCACCATCTCCAGAGACAAACGCCAAGAAACTCACTGTATCTGCAAATGAA  263
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Db    272 GAAGGGCCGATTCACCATCTCCAGAGACAAATGCCAAGAAACTCACTGTATCTGCAAATGAA  331

Qy    264 CAGCCTGAGAGCCGAGCACACGGCGGCTGTGTGTTACTACTGTGTCGGAGATTCTAGATACAGTAA  323
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Db    332 CAGCCTGAGAGACCGAGGACACGGCTGTGTATTACTGTGTCGGAGAGAATCCCATATATTGTAG  391

Qy    324 TTTCCTCCGTTGGTTCGGAGCCGACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCAT  383
          |-|||||||||| |-||          ||||||||||||||||||||||||||||||||||
Db    392 TAGTACCAGCTGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCAC  451

Qy    384 CGTCTCCTCA  393
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Db    452 CGTCTCCTCA  461
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ACCESSION   BG754024
VERSION     BG754024.1  GI:14064677
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 741)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov  row:  g  column: 14
             Plate: LLCM1686 row:  g  column: 14
             High quality sequence stop: 735.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:4846117"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_48"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT     166 a    204 c    206 g    165 t
ORIGIN

Query Match          77.0%;    Score 302.8;   DB 10;    Length 741;
Best Local Similarity 88.6%;   Pred. No. 9.4e-73;
Matches 328; Conservative   0; Mismatches  42;  Indels   0;  Gaps   0;

Qy     24 GGTGGGAGTCTGGGGGGAGGGCCTGGTCCAAGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGC  83
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     92 GGTGGGAGTCTGGGGGAGGGCTTGGTCACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC  151

Qy     84 CTCTGGATTCACCTTCACTTCAGTAGCTATATAGCAATGCACTCAGGGTCCGGGGTCCAGGGAAGG  143
          |-|||||||||||||||||||||-|||| |||| || ||||||||||||||||||||||||||||
Db    152 CTCTGGATTCACCTTCAGTAGCTATAGCAATGAACTCGGGGTCCGCGCCAGGCTTCCAGGGAAGG  211

Qy     24 GCTGGAGTGGGTCTCATCCATTAGTAAATAGTAATATTACATAATAACTACGCAACGGCAGT  203
          ||||||||||||| ||||||| ||||-|||||||||| |||||||||||||||||||||||||
Db    212 GCTGGAGTGGGTTTCATACATTAGTAGTAGTACCATATAACTACGCAGACTCTGT  271

Qy     84 GAAGGGCCGATTCACCATCTCCAGAGACAAACGCCAAGAAACTCACTGTATCTGCAAATGAA  263
          ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db    152 GAAGGGCCGATTCACCATCTCCAGAGACAAATGCCAAGAAACTCACTGTATCTGCAAATGAA  331

Qy     24 GCTGGAGTGGGTCTCATCCATTAGTAAATAGTAATATTACATAATAACTACGCAACGGCAGT  203
          ||||||||||||| ||||||| ||||-|||||||||| |||||||||||||||||||||||||
Db    212 GCTGGAGTGGGTTTCATACATTAGTAGTAGTACCATATAACTACGCAGACTCTGT  271

Qy    204 GAAGGGCCGATTCACCATCTCCAGAGACAAACGCCAAGAAACTCACTGTATCTGCAAATGAA  263
          ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db    272 GAAGGGCCGATTCACCATCTCCAGAGACAAATGCCAAGAAACTCACTGTATCTGCAAATGAA  331

Qy    264 CAGCCTGAGAGCCGAGCACACGGCGGCTGTGTGTTACTACTGTGTCGGAGATTCTAGATACAGTAA  323
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Db    332 CAGCCTGAGAGACCGAGGACACGGCTGTGTATTACTGTGTCGGAGAGAATCCCATATATTGTAG  391

Qy    324 TTTCCTCCGTTGGTTCGGAGCCGACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCAT  383
          |-|||||||||| |-||          ||||||||||||||||||||||||||||||||||
Db    392 TAGTACCAGCTGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCAC  451

Qy    384 CGTCTCCTCA  393
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Db   452 CGTCTCCTCA 461
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RESULT 3
BQ706723
BQ706723
LOCUS   BQ706723   875 bp   mRNA   linear   EST 16-JUL-2002
DEFINITION   AGENCOURT_7977332 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6215779
              5', mRNA sequence.
ACCESSION   BQ706723
VERSION   BQ706723.1   GI:21845622
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 875)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: Dr. Mark Watson
              cDNA Library Preparation: Rubin Laboratory
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLCM2385 row: d column: 20
              High quality sequence stop: 612.
FEATURES   Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6215779"
                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT   191 a   262 c   241 g   181 t
ORIGIN

Query Match   72.2%;   Score 283.6; DB 13; Length 875;
Best Local Similarity 85.4%;   Pred. No. 2e-67;
Matches   316; Conservative   0; Mismatches 54;   Indels   0; Gaps   0;

Qy   24 GGTGGAGTCTGGGGGAGGGGGAGGCCGACCCTGTCCAACCCTGGGTCCCTGAGACTTCCCGTGTGCAGC 83
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Db   134 GGTGGAGTCTGGGGGAGGCCCTGGTCAAGCCTGGGTCCCTGAGACTCTCCTGTGCAGC 193

Qy   84 CTCTGGATTCACCTTCACGTAGCTATAGCCATGCATAGCCACTGGGTCCGCCAGGGTCCAGGGAAGG 143
          |||||||||||||||||||| ||||||| ||||||||| |||||||||||||||||||||||||||||
Db   194 CTCTGGATTCACCTTCACGTATTGGCATAGAACTGGGTCCGCCAGGGTCCAGGGAAGG 253

Qy   144 GCTGGGAGTGGGTCTCATCCATTAGTAATAGATACTTACATATAACGACGACGCAGT 203
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Db   254 GCTGGGAGTGGGTCTCATCCATTAGTAGTAGCTGGCATGGAATTTCATAATTACGACGACTCAGT 313

Qy   204 GAAGGGCGAATTCACCATCTCCAGAGACAAACGCCAAGAAACTCACTGTATTGTCAAAATGAA 263
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Db   314 GAAGGGCCGAATTCACCATCTCCAGAGACAAACGCCAAGAAACTCACTGTATTGCAAAATGAA 373

Qy   264 CAGCCTGAGAGCCGAGCACACGCGCTGTTGTACTTACTGAGAGAGATCGGGAGGGCTATTA 323
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Db   374 CAGCCTGAGAGCCGAGCACACGCGGCTGTTATTACTGTCGAGAGATCGGGAGGGCTATTA 433

RESULT 4
BQ706746
BQ706746
LOCUS   BQ706746   968 bp   mRNA   linear   EST 16-JUL-2002
DEFINITION   AGENCOURT_7975960 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214709
              5', mRNA sequence.
ACCESSION   BQ706746
VERSION   BQ706746.1   GI:21845645
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 968)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: Dr. Mark Watson
              cDNA Library Preparation: Rubin Laboratory
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLCM2382 row: h column: 06
              High quality sequence stop: 522.
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                     /db_xref="taxon:9606"
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                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT   202 a   297 c   256 g   213 t
ORIGIN

Query Match   72.2%;   Score 283.6; DB 13; Length 968;
Best Local Similarity 85.4%;   Pred. No. 2.1e-67;
Matches   316; Conservative   0; Mismatches 54;   Indels   0; Gaps   0;

Qy   24 GGTGGAGTCTGGGGGAGGGGGAGGCCGACCCTGTCCAACCCTGGGTCCCTGAGACTTCCCGTGTGCAGC 83
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Db   135 GGTGGAGTCTGGGGGAGGCCCTGGTCAAGCCTGGGTCCCTGAGACTCTCCTGTGCAGC 194

Qy   84 CTCTGGATTCACCTTCAGTAGCTATAGCCATGCATAGCCACTGGGTCCGCCAGGGTCCAGGGAAGG 143
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Db   195 CTCTGGATTCACCTTCAGTAGTTATGGCATGGAATTTCATAATTACGACGACTCAGT 254

Qy   144 GCTGGGAGTGGGTCTCATCCATTAGTAATAGATACTTACATATAACGACGACGCAGT 203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   255 GCTGGGAGTGGGTCTCATCCATTAGTAGTAGCTGGCATGGAATTTCATAATTACGACGACTCAGT 314

Qy   204 GAAGGGCGAATTCACCATCTCCAGAGACAAACGCCAAGAAACTCACTGTATTGTCAAAATGAA 263
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Db   264 GAAGGGCCGAATTCACCATCTCCAGAGACAAACGCCAAGAAACTCACTGTATTGCAAAATGAA 314

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Db  315 GAAGGGCCGATTCACCATCTCCAGACAACGCCAAAGAACTCACTGTATTTGCAAATGAA 374
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Qy  264 CAGGCTGAGAGCCCAGCACACGCGTCGTGTACTACTGTGCGGAGAGATTCTAGATACAGTAA 323
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Db  375 CAGCCTGAGAGACCCGAGGAGACACGGCGTCTGTGTTACTGTGCCAGAGAGATCGGGAGGGCTATTA 434
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Qy  324 TTTCCTCCGTTGGGTTCGGAGGACGGCTCTGGGGCCCAAGGGACCACGGTCAT 383
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Db  435 CGATATTTTGACTGATTTGTCTAAAGAAACTGACTACTGGGGCCCAGGGAACCCTGGTCAC 494
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Qy  384 CGTCTCCCTCA 393
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Db  495 CGTCTCCCTCA 504
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RESULT 5
LOCUS       BX357384
DEFINITION  BX357384 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI025YF09 5-PRIME, mRNA sequence.
ACCESSION   BX357384
VERSION     BX357384.1  GI:30366120
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 889)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr; Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 7198.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI025CCO5QP1&cluster=7198.r. Contact :
            Feng Liang Email : fliang@lifetech.com
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI025CCO5QP1.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /clone="CS0DI025YF09"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT  200 a  252 c  251 g  184 t  2 others
ORIGIN
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Query Match          71.8%;  Score 282;  DB 13;  Length 889;
Best Local Similarity 87.3%;  Pred. No. 5.7e-67;
Matches 323; Conservative 0; Mismatches 40; Indels 7; Gaps 1;

Qy   24 GGTGGAGTCTGGGGGAGGCCTGGTGTCAAGCCTGGGGGGTCCCTGAGACTCTCCGTTGCAGC 83
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Db  179 GGTGGAGTCTGGGGGAGGCTTGGTGTACAGCCTGGGGGGTCCCTGAGACTCTCTGTGCAGC 238
Qy   84 CTCTGGATTCACCTTCACGTAGCTATAGCTATATGAGCATGACACCCTGAGACTCTCACTGTCAGGGAAGGG 143
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Qy  144 GCTGGAGTGGGGTGGTCTCATCCATTAGTAATAGTAATTACTTACATATAACTGACGACCGAGT 203
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Db  144 GGTGGAGTCTGGGGGAGGCCTGGGGGGAGGGGCGTCAAGGCCTCGTGGGTTCAGC 203
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Db  299 GCTGGAGTGGGGTTCATACAATTAGTAGTAGTGGTAGTACCATATACGACAGACTCTGT 358
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Qy  204 GAAGGGCCGATTCACCATCTCCAGACAACGCCAAGGAACTCACTGTATCTGCAAAATGAA 263
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Db  359 GAAGGGCCGATTCACCATCTCCAGACAACGCCAAGAAACTCACTGTATCTGCAAAATGAA 418
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Qy  264 CAGGCTGAGAGCCCAGCACACGCGTCGTGTACTACTGTGCGGAGAGATTCTAGATACAGTAA 323
        ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db  419 CAGCCTGAGAGACGAAGGACACGGCGTCTGTGTTACTCTGCCAGAGATTAGGTA------TCT 471
        |||||||||| ||||| ||||||||| ||||| ||||||||||| |||| |||
Qy  324 TTTCCTCCGTTGGGTTCGGAGGACGGCTATGGAGCCCAAGGGACCACGGTCAT 383
        |||||| || |||||||||||||||| ||||| |||| |||||||||
Db  472 TTGGCGCAGGTGGTGTACACCCTGGGACGGTTATGGAGGTCTGGGGCCCAAGGGACCACGGTCAC 531
        ||||| |||||||||| |||||
Qy  384 CGTCTCCCTCA 393
        |||||||||||
Db  532 CGTCTCCCTCA 541
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```
RESULT 6
LOCUS       BQ711355
DEFINITION  BQ711355 AGENCOURT_8353131 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278123
            5', mRNA sequence.
ACCESSION   BQ711355
VERSION     BQ711355.1  GI:21850254
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1004)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2465  row: j  column: 12
            High quality sequence stop: 486.
FEATURES             Location/Qualifiers
     source          1..1004
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6278123"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT  217 a  299 c  279 g  209 t
ORIGIN
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Query Match          71.7%;  Score 281.8;  DB 13;  Length 1004;
Best Local Similarity 86.6%;  Pred. No. 6.9e-67;
Matches 323; Conservative 0; Mismatches 47; Indels 3; Gaps 1;

Qy   24 GGTGGAGTCTGGGGGAGGCCTGGTGTCAAGCCTGGTGGGTTCCCTGAGACTCTCCGTTGCAGC 83
        |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db  130 GGTGGAGTCTGGGGGAGGCCTGGGGGGAGGGGCGTCAAGGCCTCGTGGGTTCAAGCCTCGTCAAGACTCTCCTGTGCAGC 189
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```
RESULT 7
BQ711025
LOCUS       BQ711025              1010 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_7983315 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6215468
            5', mRNA sequence.
ACCESSION   BQ711025
VERSION     BQ711025.1  GI:21849924
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1010)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2384 row: g column: 21
            High quality sequence stop: 358.
FEATURES             Location/Qualifiers
     source          1..1010
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6215468"
                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
```

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Qy    84 CTCTGGATTCACCTTCAGTAGTCTATAGCATGCACTGGGTCCGCCGCCAGGGTCCAGGGAAGG 143
         |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   190 CTCTGGATTCACCTTCAGTAGTCTATAGCATGAACTGGGTCCGCCGCCAGGGTCCAGGGAAGG 249

Qy   144 GCTGGAGTGGGGTCTCATCCATTAGTAATACTTACATATACTACGCACAGACGCAGT 203
         |||||||||||||||||  || |  |||    ||||||||||||||||||| |||||
Db   250 GCTGGAGTGGGGTCTCATTGTAGTAGTACTTACATATACTACGCACAGACGCAGT 309

Qy   204 GAAGGGCCGATTCACCATCTCCAGAGACANCAAGCAACCCAGAAGAACTCACTGTATGCAAATGAA 263
         ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db   310 GAAGGGCCGATTCACCATCTCCAGAGACAACAAGCAACCCAGAAGAACTCACTGTATGCAAATGAA 369

Qy   264 CAGCCTGAGAGCCGAGACACGCGTGTCTACTACTGTGCGAGAGATTCTAGATACAG---320
         |||||||||||||||||||||||  || |  ||||||||||||||||||||||||
Db   370 CAGCCTGAGAGCCGAGACACGCGTCTGTATTACTGTGCGAGAGACGGGTGGAGGGGGCT 429

Qy   321 TAATTTCCTCCGTTGGGTTCGGAGCACACGGTATGGACGGTATCTGGGGCCAAGGGACCACGGT 380
         ||  |  | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   430 ACTATGGTTCGGGGGGGGGCGACAAAATATGATGCTTTTGATATCTGGGGCCAAGGGACAATGGT 489

Qy   381 CATCGTCTCCTCA 393
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Db   490 CACCGTCTCTTCA 502
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BASE COUNT      202 a     301 c     272 g     235 t
ORIGIN
Query Match       70.7%;   Score 277.8;   DB 13;   Length 1010;
Best Local Similarity   84.6%;   Pred. No. 8.7e-66;
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Matches 312;  Conservative  0;  Mismatches 57;  Indels  0;  Gaps  0;

RESULT 8
BG397964
LOCUS       BG397964              687 bp    mRNA    linear   EST 12-MAR-2001
DEFINITION  602439484F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4565804 5',
            mRNA sequence.
ACCESSION   BG397964
VERSION     BG397964.1  GI:13291412
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 687)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1283 row: g column: 21
            High quality sequence stop: 673.
FEATURES             Location/Qualifiers
     source          1..687
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4565804"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_48"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Library constructed by Ling
                     for average insert size 1.8kb. Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
```

```
Qy    24 GGTGGAGTCTGGGGGAGGCGTTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    75 GGTGGAGTCTGGGGGAGGCGTTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 135

Qy    84 CTCTGGATTCACCTTCAGTAGCTATAGGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG 143
         ||||||||||||||||||||| |||||| ||||||||||||||||||||||||||||||||
Db   135 CTCTGGATTCACCTTCAGTAGTTATAATATGGCATGGAACTGGGTCCGCCAGGCTCCAGGGAAGG 194

Qy   144 GCTGGAGTGGGGTCTCATCCATTAGTAATAGTAATACTTACATATACTACGCACAGACGCAGT 203
         |||||||||||| || | || | |   |   || |  |||||||||||||||||||||||||
Db   195 GCTGGAGTGGGGTCTCATTGATAGTAGTAGTAGTACTTACATATACTACGCACAGACGCAGT 254

Qy   204 GAAGGGCCGATTCACCATCTCCAGAGACAAGCAAGCAACCCAGAAGAACTCACTGTATGCAAATGAA 263
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   255 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCTCTGTATTGCAAATGAA 314

Qy   264 CAGCCTGAGAGCCGAGACACGCGTGTCTACTACTGTGTGCGAGAGATTCTAGATACAGTAA 323
         |||||||||||||||||||||| | ||||||||| | | |  | || |  | |  ||| |
Db   315 CAGCCTGAGAGCCGAGACACGGGTCTGTATTACTGTGCGAGAGATCGGTAGTATACAGTAA 374

Qy   324 TTTCCCGCGTTGGGGTTCGGGGACCAAGGGACCACGGTCTGGGGGCCAAGGGACCACGGTCAT 383
         ||| | |  ||||||||||||||| ||||||||||||| |||||||||||||||||||||
Db   375 CAGCCTGAGAGCCGAGACACGGGTCTGTATTACTGTGCGATTTA 434

Qy   384 CGTCTCCTC 392
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Db   495 CGTCTCCTC 503
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RESULT 9

BM914329

LOCUS   BM914329   1069 bp   mRNA   linear   EST 12-MAR-2002
DEFINITION AGENCOURT_6615320 NIH_MGC_113 Homo sapiens cDNA clone
            5', mRNA sequence.
ACCESSION   BM914329
VERSION   BM914329.1 GI:19364708
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1069)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2002 row: c column: 05
            High quality sequence stop: 556.

FEATURES   Location/Qualifiers
     source   1..1069
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5479996"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."

BASE COUNT   147 a   189 c   197 g   154 t

ORIGIN

Query Match   69.5%;   Score 273.2; DB 10; Length 687;
Best Local Similarity   97.2%; Pred. No. 1.3e-64;
Matches 278; Conservative   0; Mismatches 8; Indels   0; Gaps   0;

Qy   24 GGTGGAGTCTGGGGGGAGGGCCTGGTGTCAAGCCTCGGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   116 GGTGGAGTCTGGGGGGAGGGCCTGGTGTCAAGCCTCGGGGGGGTCCCTGAGACTCTCCTGTGCAGC 175

Qy   84 CTCTGGATTCACCTTCAGTAGATCACTGGGGTCCGCCGCCAGGGGTTCCCAGGGGAAGGG 143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   176 CTCTGGATTCACCTTCAGTAGCTATAGACATGAAGCTGGGGTCCGCCGCCAGGGGTTCCCAGGGGAAGGG 235

Qy   144 GCTGGAGTGGGGTCTCATCCATTAGTAATAGTAATACTTACATATATACTACCGCAGCAGT 203
          ||||||||||||||||||||||||||| ||||||||||||||||||||||| ||||||
Db   236 GCTGGAGTGGGGTCTCATCCATTAGTAGTAGTTACATATACTACGCAGCAGACTCAGT 295

Qy   204 GAAGGGCCGATTCACCATCTCCAGAGACAAACGCCAAGAACTCACTGTGTATCTGCAAAATGAA 263
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   296 GAAGGGCCGATTCACCATCTCCAGAGAACAACGCCAAGAACTCACTGTATCTGCAAAATGAA 355

Qy   264 CAGCCTGAGAGCCGAGCACACGGCTGTGTGTACTACGTGGGAGAGAT 309
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   356 CAGCCTGAGAGCCGAGCACACGGCTGTGTATTACGTGCCGAGAGAT 401

RESULT 10

AW403220

LOCUS   AW403220   471 bp   mRNA   linear   EST 16-FEB-2000
DEFINITION UI-HF-BK0-aay-h-04-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
            IMAGE:3055710 5', mRNA sequence.
ACCESSION   AW403220
VERSION   AW403220.1 GI:6922096
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 471)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: M.B. Soares Lab
            cDNA Library Arrayed by: M.B. Soares Lab
            DNA Sequencing by: M.B. Soares Lab
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.

FEATURES   Location/Qualifiers
     source   1..471
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3055710"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /clone_lib="NIH_MGC_36"
                     /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (0.5-1.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT   98 a   127 c   143 g   103 t

BASE COUNT   268 a   362 c   262 g   176 t   1 others

ORIGIN

Query Match   68.7%;   Score 270; DB 12; Length 1069;
Best Local Similarity   96.5%; Pred. No. 1.3e-63;
Matches 276; Conservative   0; Mismatches 10; Indels   0; Gaps   0;

Qy   24 GGTGGAGTCTGGGGGGAGGGCCTGGTGTCAAGCCTCGGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   126 GGTGGAGTCTGGGGGGAGGGCCTGGTGTCAAGCCTCGGGGGGGTCCCTGAGACTCTCCTGTGCAGC 185

Qy   84 CTCTGGATTCACCTTCAGTAGCTATAGACATGACACTGGGGTCCGCCGCCAGGGGTTCCCAGGGGAAGGG 143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   186 CTCTGGATTCACCTTCAGTAGCTATAGACATGAAGCTGGGGTCCGCCGCCAGGGGTTCCCAGGGGAAGGG 245

Qy   144 GCTGGAGTGGGGTCTCATCCATTAGTAATAGTAATACTTACATATATACTACCGCAGCAGT 203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   246 GCTGGAGTGGGGTCTCATCGATGAGTAGTAGTTACATATACTACGCAGCAGACTCAGT 305

Qy   204 GAAGGGCCGATTCACCATCTCCAGAGACAAACGCCAAGAACTCACTGTGTATCTGCAAAATGAA 263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   306 GAAGGGCCGATTCACCATCTCCAGAGACAAACGCCAAGAACTCACTGTATCTGCAAAATGAA 365

Qy   264 CAGCCTGAGAGCCGAGCACACGGCTGTGTGTTACTACGTCCGAGAGAT 309
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   366 CAGCCTGAGAGCCGAGCACACGGCTGTGTATTACGTGTCGGAGAGAT 411

RESULT 11

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BG686881
LOCUS       BG686881                908 bp    mRNA    linear   EST 01-MAY-2001
DEFINITION  602650867F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4763153 5',
            mRNA sequence.
ACCESSION   BG686881
VERSION     BG686881.1  GI:13918278
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 908)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1618 row: f  column: 18
            High quality sequence stop: 899.
FEATURES             Location/Qualifiers
     source          1..908
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4763153"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /clone_lib="NIH_MGC_48"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      200 a    262 c    250 g    194 t    2 others
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Query Match 68.2%;  Score 268.2;  DB 9;  Length 471;
Best Local Similarity 93.9%;  Pred. No. 2.5e-63;
Matches 279;  Conservative 0;  Mismatches 18;  Indels 0;  Gaps 0;

Qy   24 GGTGGAGTCTGGGGGAGGAGGCTCGGTCAAGCCTCTGGGGGTCCCTGAGACTCTCCTTGTCGAGC 83
         ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db   87 GGTGGAGTCTGGGGGAGGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTTGTCGAGC 146

Qy   84 CTCTGGATTCACCTTCAGTAGCTATACCATGCACTGGGTCTCCCCGCCCAGGGTCCAGGGAAGG 143
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 CTCTGGATTCACCTTCAGTAGGCGGATACCATGAACTGGGTCTCCCCAGGGTCCAGGGAAGG 206

Qy  144 GCTGGGAGTGGGGTCTCATCCATTAGTAATATAGTTAACATTAACACTACGGCACGACCGCAGT 203
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  207 GCTGGGAGTGGGGTCTCACCCATTAGTAATAGTTAATATTCATTACTACTACGGCACGACTCAGT 266

Qy  204 GAAGGGGCCGATTCACCAATCTCCAGAGACAACCGCCAAGAACTCACTGTATCTGCAAATGAA 263
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Db  267 GAAGGGCCGATTCACCAATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 326

Qy  264 CAGCCTGAGAGCCGAGCACACGGCTGTTGTGTACTACTGGTACTACTGTGCGAG 320
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Db  327 CAGCCTGAGAGCCGAGCACACGGCTGTGTTATTACTGTGCGAGAGCCCATAGTAGCAG 383
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RESULT 12

```
AW403886
LOCUS       AW403886                397 bp    mRNA    linear   EST 16-FEB-2000
DEFINITION  UI-HF-BK0-abo-d-09-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
            IMAGE:3057064 5', mRNA sequence.
ACCESSION   AW403886
VERSION     AW403886.1  GI:6923039
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 397)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: M.B. Soares Lab
            cDNA Library Arrayed by: M.B. Soares Lab
            DNA Sequencing by: M.B. Soares Lab
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1..397
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3057064"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /clone_lib="NIH_MGC_36"
                     /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (0.5-1.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT       87 a     92 c    120 g     98 t
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Query Match 68.2%;  Score 268.2;  DB 10;  Length 908;
Best Local Similarity 96.8%;  Pred. No. 3.7e-63;
Matches 273;  Conservative 0;  Mismatches 9;  Indels 0;  Gaps 0;

Qy   24 GGTGGAGTCTGGGGGAGGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTTGTCGAGC 83
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  139 GGTGGAGTCTGGGGGAGGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTTGTCGAGC 198

Qy   84 CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCTCCCCGCCCAGGGTCCAGGGAAGG 143
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  199 CTCTGGATTCACCTTCAGTAGCTATAGCATGAACTGGGTCTCCCCAGGGTCCAGGGAAGG 258

Qy  144 GCTGGGAGTGGGGTCTCATCCATTAGTAATATAGTTAATATTCATTACTACTACGGCACGACCGCAGT 203
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  259 GCTGGGAGTGGGGTCTCATCCATTAGTAATAGTTAATATTCATTACTACTACGGCACGACTCAGT 318

Qy  204 GAAGGGGCCGATTCACCAATCTCCAGAGACAACCGCCAAGAACTCACTGTATCTGCAAATGAA 263
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  319 GAAGGGCCGATTCACCAATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 378

Qy  264 CAGCCTGAGAGCCGAGCACACGGCTGTTGTGTACTACTGTGCGAG 305
         |||||||||||||||||||||||||||||||||||||||||||||
Db  379 CAGCCTGAGAGCCGAGCACACGGCTGTTGTGTATTACTGTGCGAG 420
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Query Match
Best Local Similarity    68.0%;    Score 267.4;  DB 9;  Length 397;
Matches 280;  Conservative   0;  Pred. No. 3.9e-63;  Mismatches 21;  Indels  0;  Gaps  0;

Qy    24 GGTGGAGTCTGGGGAGGGCCTGGTCAAGCCTGGGGGGTTCCCTGAGACTTCTCCGTGTGCAGC 83
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    88 GGTGGAGTCTGGGGAGGGCCTGGTCAAGCCTGGGGGGTTCCCTGAGACTTCTCCGTGTGCAGC 147

Qy    84 CTCTGGATTCACCTTCAGTAGCTATATAGCATGCACTGGGTCTCCGCCAGGTCCAGGGAAGGG 143
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   148 CTCTGGATTCACCTTCAGTAGCTATATAGCATGCACTGGGTCTCCGCCAGGTCCAGGGAAGGG 207

Qy   144 GCTGGAGTGGGTGTTCATCCATTAGTAATAGTAATACTTACGCAGCAGGCAGT 203
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   208 GCTGGAGTGGGTGTCTCATCCATTAGTAGTAGTTACATAATACTACGCAGACTCAGT 267

Qy   204 GAAGGGCCGATTCACCATCTCCAGAGACAAACGCCAAGAAACTCACTGTATCTGCAAATGAA 263
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   268 GAAGGGCCGATTCACCATCTCCAGAGACAACTCACTGTATCTGTATCTGCAAATGAA 327

Qy   264 CAGCCTGAGAGCGGCAGCACACGCCGTCGTACTTCTGTCGGAGAGATTCTTAGATACACGTAA 323
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   328 CAGCCTCAGAGCCCAGGACACGGCTGTGTTGTTATTACTGTGCCGAGGAAATTATATTGTAC 387

Qy   324 T 324
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Db   388 T 388
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RESULT 13
BX379829
LOCUS   BX379829   1138 bp   mRNA   linear   EST 08-MAY-2003
DEFINITION   BX379829 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
               clone CS0DI040YE16 5-PRIME, mRNA sequence.
ACCESSION   BX379829
VERSION   BX379829.1   GI:30454789
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1138)
  AUTHORS   Li,W.B.; Gruber,C.; Jessee,J. and Polayes,D.
  TITLE   Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
COMMENT   Contact: Genoscope
               Genoscope - Centre National de Sequencage
               BP 191 91006 EVRY cedex - France
               Email: seqref@genoscope.cns.fr; Web : www.genoscope.cns.fr
               Library was constructed by Life Technologies, a division of
               Invitrogen. This sequence belongs to sequence cluster 7198.r For
               more information about this cluster, see
               http://www.genoscope.cns.fr/
               cgi-bin/cluster.cgi?seq=CS0DI040BC080P1cluster=7198.r Contact :
               Feng Liang Email : fliang@lifetech.com URL :
               http://fullength.invitrogen.com/ InvitroGen Corporation 1600
               Faraday Avenue Genoscope sequence ID : CS0DI040BC08QP1.
FEATURES   Location/Qualifiers
     source   1..1138
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI040YE16"
                     /tissue_type="PLACENTA"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT   250 a   323 c   329 g   225 t   11 others
ORIGIN

Query Match   67.9%;   Score 266.8;   DB 13; Length 1138;

Best Local Similarity   86.5%;   Pred. No. 1e-62;
Matches 320; Conservative   0; Mismatches 17; Indels 33; Gaps 1;

Qy   24 GGTGGAGTCTGGGGAGGGCCTGGTCAAGCCTGGGGGGTTCCCTGAGACTTCTCCGTGTGCAGC 83
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   197 GGTGGAGTCTGGGGAGGGCCTGGTCAAGCCTGGGGGGTTCCCTGAGACTTCTCCGTGTGCAGC 256

Qy   84 CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCTCCGCCAGGTCCAGGGAAGGG 143
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   257 CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCTCCGCCAGGTCCAGGGAAGGG 316

Qy   144 GCTGGAGTGGGTGTTCATCCATTAGTAATAGTAATACTTACACATAATACGCAGCAGGCAGT 203
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   317 GCTGGAGTGGGTGTCTCATCCATTAGTAGTAATAATACATATACACATAATACGCAGACTCAGT 376

Qy   204 GAAGGGCCGATTCACCATCTCCAGAGACAAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   377 GAAGGGCCGATTCACCATCTCCAGAGACAACTCACTGTATCTGTATCTGCAAATGAA 436

Qy   264 CAGCCTGAGAGCGGCAGCACACGCCGTCGTGTACTTCTGTCGGAGAGATTCTTAGATACACGTAA 323
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   437 CAGCCTGAGAGCCCAGGACACGGCTGTGTTGTTATTACTGTGCCGAGAG 480

Qy   324 TTTCCTCCGTTGGGTTCCGGACGCGACGGTATTGGACGGTCTGGGGCCCAAGGGACCACGGTCAT 383
                         |||||||||||||||||||||||||||
Db   481 ------------------GGGGTACGGTATTGGACGTCTGGGGCCCAAGGGACCACGGTCAC 523

Qy   384 CGTCTCCTCA 393
         ||||||||||
Db   524 CGTCTCCCCA 533
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RESULT 14
BX417408
LOCUS          BX417408          1201 bp          mRNA          linear          EST 13-MAY-2003
DEFINITION     BX417408 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE009YI15
               5-PRIME, mRNA sequence.
ACCESSION      BX417408
VERSION        BX417408.1    GI:30650401
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
  ORGANISM     Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1  (bases 1 to 1201)
  AUTHORS      Li,W.B.; Gruber,C.; Jessee,J. and Polayes,D.
  TITLE        Full-length cDNA libraries and normalization
  JOURNAL      Unpublished
COMMENT        Contact: Genoscope
               Genoscope - Centre National de Sequencage
               BP 191 91006 EVRY cedex - France
               Email: seqref@genoscope.cns.fr; Web : www.genoscope.cns.fr
               Library was constructed by Life Technologies, a division of
               Invitrogen. This sequence belongs to sequence cluster 7198.r For
               more information about this cluster, see
               http://www.genoscope.cns.fr/
               cgi-bin/cluster.cgi?seq=CS0DE009AE08QP1cluster=7198.r Contact :
               Feng Liang Email : fliang@lifetech.com URL :
               http://fullength.invitrogen.com/ InvitroGen Corporation 1600
               Faraday Avenue Genoscope sequence ID : CS0DE009AE08QP1.
FEATURES             Location/Qualifiers
     source          1..1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DE009YI15"
                     /tissue_type="PLACENTA"
                     /clone_lib="Homo sapiens PLACENTA"
                     /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
                     with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-strand cDNA was digested with Not I and cloned into
                     the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                     Library was not normalized."

RESULT 15

```
LOCUS       AW402793                447 bp    mRNA    linear   EST 16-FEB-2000
DEFINITION  UI-HF-BK0-aaq-a-05-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
            IMAGE:3054608 5', mRNA sequence.
ACCESSION   AW402793
VERSION     AW402793.1  GI:6921535
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 447)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: M.B. Soares Lab
            cDNA Library Arrayed by: M.B. Soares Lab
            DNA Sequencing by: M.B. Soares Lab
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1..447
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3054608"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
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BASE COUNT       266 a    331 c    324 g    240 t    40 others
ORIGIN

Query Match           67.9%;  Score 266.8;  DB 13;  Length 1201;
Best Local Similarity 86.5%;  Pred. No. 1e-62;
Matches 320; Conservative 0; Mismatches 17; Indels 33; Gaps 1;

Qy     24 GGTGGAGTCTGGGGAGGCCCTGGTCAAGCCCTGGGGGGTCCCTTGAGACTCTCCTGTGCAGC 83
          ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    206 GGTGGAGTCTGGGGAGGCCTGGTCAAGCCCTGGGGGGTCCCTTGAGACTCTCCTGTGCAGC 265

Qy     84 CTCTGGATTCACCTTCAGTAGCTATAGCCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG 143
          |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    266 CTCTGGATTCACCTTCAGTAGCTATAACATGAACTGGGTCCGCCAGGCTCCAGGGAAGGG 325

Qy    144 GCTGGAGTGGGTGTCATCCATTAGTAATAGTAATAGTATACATATATACGCGAGACACGCAGT 203
          |||||||||||| ||| |||| |||||| |||||||| ||||||||||||||||||||||
Db    326 GCTGGAGTGGGTCTCATCCATTAGTAGTAATAGTGGTTACATAATATACTACGCAGACTCAGT 385

Qy    204 GAAGGCCCGATTCACCATCTCCAGAGACAACAAGCGCCAAGACAGAACTCACTGTATCTGCAAATGAA 263
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db    386 GAAGGCCCGATTCACCATCTCCAGAGACAACAACTCACCAAGACAGAACTCACTGTATCTGCAAATGAA 445

Qy    264 CAGCCTGAGAGCCGAGCCACACGGGCTGTGTTACTACTGTGCGAGAGGATTCTTAGATACAGTAA 323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db    446 CAGCCTGAGAGCCGAGGACACGGGCTGTGTTATTACTGTGCGAGAG-----------GGAGAG 489

Qy    324 TTTCCTCCGTTCGGGTTCGGAGGCGACGTATGAGACGTGTGGGCCGCCAAGGGACCACGGTTCAT 383
           || |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    490 -----------GGGGTACGGTATGGACGTGTGGGCCGCCAAGGGACCACGGTTCAC 532

Qy    384 CGTCTCCTCA 393
          |||||| |||
Db    533 CGTCTCCCCA 542
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RESULT 16

```
LOCUS       BG340686                738 bp    mRNA    linear   EST 27-FEB-2001
DEFINITION  602462268F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4575041 5',
            mRNA sequence.
ACCESSION   BG340686
VERSION     BG340686.1  GI:13147124
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 738)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1285 row: h column: 18
            High quality sequence stop: 733.
FEATURES             Location/Qualifiers
     source          1..738
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4575041"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_48"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
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BASE COUNT       110 a    137 c    137 g    103 t
ORIGIN

Query Match            97 a
Best Local Similarity 67.2%;  Score 264;  DB 9;  Length 447;
Matches 276; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy     24 GGTGGAGTCTGGGGAGGCCCTGGTCAAGCCCTGGGGGGTCCCTTGAGACTCTCCTGTGCAGC 83
          ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    106 GGTGGAGTCTGGGGAGGCCTGGTCAAGCCCTGGGGGGTCCCTTGAGACTCTCCTGTGCAGC 165

Qy     84 CTCTGGATTCACCTTCAGTAGCTATAGCCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG 143
          |||||||||||||||||||||||||| || |||||||||||||||||||||||||||||||
Db    166 CTCTGGATTCAGCTTCAATAGCTACACCATGAACTGGGTCCGCCAGGCTCCAGGGAAGGG 225

Qy    144 GCTGGAGTGGGTGTCATCCATTAGTAATAGTAATAGTATACATATATACGCGAGACACGCAGT 203
          ||||||||||||| |||||| |||||| ||||||| ||||||||||||||||||||||||
Db    226 GCTGGAGTGGGTCTCATCCATTAGTAGTAATAGTGGTTAGTTACATAATATATTACGCAGACTCAGT 285

Qy    204 GAAGGCCCGATTCACCATCTCCAGAGACAACAAGCGCCAAGACAGAACTCACTGTATCTGCAAATGAA 263
          |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db    286 GAAGGCCCGATTCACCATCTCCAGAGACAACAACTCACTGTATCTGCAAATGAA 345

Qy    264 CAGCCTGAGAGCCGAGGCCACACGGCTGTGTGTTACTACTGTGCGAGAGATTCTAGATACA 319
          |||||||||||||||||| |||||||||||||||||||||||||||||| ||||
Db    346 CAGCCTGAGAGCCAGGACACGGCTGTGTTATTACTGTGCGAGAGATTTGTCCTACA 401
```

RESULT 17

```
LOCUS       BM007475       613 bp    mRNA    linear    EST 30-OCT-2001
DEFINITION  603616742F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5440475 5',
            mRNA sequence.
ACCESSION   BM007475
VERSION     BM007475.1  GI:16521829
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 613)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1913 row: d  column: 12
            High quality sequence stop: 608.
FEATURES             Location/Qualifiers
     source          1..613
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5440475"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT    156 a   207 c   213 g   161 t
ORIGIN

Query Match     67.0%;    Score 263.2;  DB 10;  Length 738;
                                                            1 others
Best Local Similarity  96.9%;    Pred. No. 7.8e-62;
Matches  279;  Conservative  0;  Mismatches  8;  Indels  1;  Gaps  1;

Qy   24 GGTGGAGTCTGGGGAGGAGGCCCTGGTCAAGGCCTGGAGGGGGGGTCCCTGAGACTCTCCTGTGCCAGC 83
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  134 GGTGGAGTCTGGGGAGGAGGCCCTGGTCAAGGCCTGGAGGGGGGGTCCCTGAGACTCTCCTGTGCCAGC 193

Qy   84 CTCTGGATTCACCTTCAGTAGCTATAGCATCCACTGGGTGGGGGTCCCGCCCAGGGTCCAGGGAAGGG 143
         ||||||||||||||||||||||||||||||    ||||||  |||||||||||||||||  |||||||
Db  194 CTCTGGATTCACCTTCAGTAGCTATAGCATGAACTGGGTCCCGCCCAGGGTCCA-GGAAGGG 252

Qy  144 GCTGGAGTGGGTCTCATCCATTAGTAATATACTTACATATAACTTACGCAGACGCGAGT 203
         |||||||||| ||||||||||||||| |||  |||||||||||||  |||| |  |||||
Db  253 GCTGGAGTGGGGTCTCATCCATTAGTAGTAGTTACATATAACTTACGGAGACTCAGT 312

Qy  204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAAACTCACTGTATCTGCAAATGAA 263
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  313 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAAACTCACTGTATCTGCAAATGAA 372

Qy  264 CAGCCTGAGAGCCGAGCACACACGGCGTGTGTATTACTGTGCGAGAGATTC 311
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  373 CAGCCTGAGAGCCGAGCACACACGGCGTGTGTATTACTGTGCGAGAGATTC 420
```

RESULT 18

```
LOCUS       BG759748       879 bp    mRNA    linear    EST 15-MAY-2001
DEFINITION  6027111146F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4851587 5',
            mRNA sequence.
ACCESSION   BG759748
VERSION     BG759748.1  GI:14070401
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 879)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1694 row: k  column: 12
            High quality sequence stop: 879.
FEATURES             Location/Qualifiers
     source          1..879
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4851587"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_48"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using GGCACGAG(G). Size-selected
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling

BASE COUNT    126 a   172 c   174 g   141 t
ORIGIN

Query Match     65.8%;    Score 258.4;  DB 12;  Length 613;
Best Local Similarity  94.4%;    Pred. No. 1.5e-60;
Matches  268;  Conservative  0;  Mismatches  16;  Indels  0;  Gaps  0;

Qy   24 GGTGGAGTCTGGGGAGGAGGCCCTGGTCAAGGCCTGGGGGGGGGTCCCTGAGACTCTCCTGTGCCAGC 83
         |||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db  132 GGTGGAGTCTGGGGAGGAGGCCCTGGTCAAGGCCTGGAGGGGGGGTCCCTGAGACTCTCCTGTGCCAGC 191

Qy   84 CTCTGGATTCACCTTCAGTAGCTATAGCATGAACTGGGTCCCGCCCAGGGTCCAGGGAAGGG 143
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Qy  144 GCTGGAGTGGGTCTCATCCATTAGTAATATACTTACATATAACTTACGCAGACGCGAGT 203
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Db  252 GCTGGAGTGGGGTCTCATCCATTAGTAGTAGTTACATATAACTTACGGAGACTCAGT 311

Qy  204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAAACTCACTGTGTCTGCAAATGAA 263
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Db  312 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAAACTCACTGTGTCTGCAAATGAA 371

Qy  264 CAGCCTGAGAGCCGAGCACACACGGCGTGTGTATTACTGTGCGAGG 307
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Db  372 CAGCCTGAGAGCCGAGCACACACGGCGTGTTTATTACTGTGCGAGG 415
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RESULT 19
BQ709879
LOCUS   BQ709879   890 bp   mRNA   linear   EST 16-JUL-2002
DEFINITION AGENCOURT_8354557 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281260
            5', mRNA sequence.
ACCESSION   BQ709879
VERSION   BQ709879.1 GI:21848778
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 890)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2473 row: m column: 05
            High quality sequence start: 11
            High quality sequence stop: 564.
FEATURES   Location/Qualifiers
     source   1..890
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6281260"
                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC library."

BASE COUNT   181 a   280 c   238 g   180 t
ORIGIN

Query Match   65.8%; Score 258.4; DB 10; Length 879;
Best Local Similarity   94.4%; Pred. No. 1.8e-60;
Matches 268; Conservative   0; Mismatches 16; Indels   0; Gaps   0;

Qy   24 GGTGGGAGTCTGGGGGAGGCCTGGTCTCAAGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
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Qy   84 CTCTGGATTCACCTTCAGTAGCTGTATAGAGCATGACTGGGGTCCGCCCAGGGGTCCAGGGAAGG 143
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Qy   144 GCTGGAGTGGGGTCTCATCCCATTAGTAAATAATACTTTACATATNATACGCACAGACGCAGT 203
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Db   258 GCTGAAGTGGGGTCTCATGTATTAGTAGTAGTAGTCACATATNCCTACGCACAGACTCTGT 317

Qy   204 GAAGGGCCGATTCACCATTCTCCAGAGACAACGCCAAGAAACTCACTGTATCTGCAAATGAA 263
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   318 GAAGGGCCGATTCACCATTCTCCAGAGACAACGCCAAGAAACTCACTGTATCTGCAAATGAA 377

Qy   264 CAGCCTGAGAGACCGAGCCGAGGACACACGGCTGTGTGTACTACTGTGCCGAGAG 307
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Db   378 CAGCCTGAGAGACCGAGGACACGGCGCTGTCTGTATTACTGTGCGAGAG 421

RESULT 20
AW401428
LOCUS   AW401428   443 bp   mRNA   linear   EST 16-FEB-2000
DEFINITION UI-HF-BK0-aad-b-02-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
            IMAGE:3053139 5', mRNA sequence.
ACCESSION   AW401428
VERSION   AW401428.1 GI:6920011
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 443)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: M.B. Soares Lab
            cDNA Library Arrayed by: M.B. Soares Lab
            DNA Sequencing by: M.B. Soares Lab
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
FEATURES   Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3053139"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /clone_lib="NIH_MGC_36"
                     /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (0.5-1.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima

BASE COUNT   192 a   279 c   240 g   178 t   1 others
ORIGIN

Query Match   65.5%; Score 257.4; DB 13; Length 890;
Best Local Similarity   92.8%; Pred. No. 3.4e-60;
Matches 270; Conservative   0; Mismatches 21; Indels   0; Gaps   0;

Qy   24 GGTGGAGTCTGGGGGAGGCCTGGTCTCAAGCCCTGGGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
          ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   129 GGTGGAGTCTGGGGGAGGCCTGGTCTCAAGCCTGGGGGGGGTCCCTGAGACTCTCCTGTGCAGC 188

Qy   84 CTCTGGATTCACCTTCAGTAGCTATAGAGCATGACTGGGGTCCGCCCAGGGGTCCAGGGAAGG 143
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   189 CTCTGGATTCCCTACAGTAGTTATACCAGTAGTAAGCATGGGGTCCGCCCAGGGGTCCAGGGAAGG 248

Qy   144 GCTGGAGTGGGGTCTCATCCCATTAGTTAATAATAGTAATACTTACATATATACGCAGACGCAGT 203
          ||||| || ||||||||| |||||||||| ||||||||||| |||| ||||| |||||||| |||
Db   249 GCTAGATTGGGGTCCTCATCCCATTAGTGGTACTACTAGTTACATATAACTACTACGCCAGACTCAGT 308

Qy   204 GAAGGGCCGATTCACCATTCTCCAGAGACAACGCCAAGAAACTCACTGTATCTGCAAATGAA 263
          |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db   309 GAAGGGCCGATTCACCATTCTCCAGAGACAACGCCAAGAAACTCACTGTATTGCAAATGAA 368

Qy   264 CAGCCTGAGAGACCGAGCCGAGGACACACGGCTGTGTACTACTGTGCGAGAGATGGTTCTAG 314
          ||||||||||||||||||||||||||||||||||||||| || |||||||||||||| |||
Db   369 CAGCCTGAGAGACCGAGGACACGGCGTCTGTTTATTACTGTGCCGAGAGATGGGGAG 419

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BASE COUNT       93 a   116 c   131 g   103 t
ORIGIN
                 Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

Query Match      65.3%;   Score 256.8;  DB 9;   Length 443;
Best Local Similarity   94.0%;   Pred. No. 3.4e-60;
Matches  267;  Conservative   0;  Mismatches  17;  Indels   0;  Gaps   0;

Qy     24 GGTGGGAGTCTGGGGGAGGGCCTGGTCAAGCCTGGGGGGTCCCTGAGGACTCTCCTGTGCAGC      83
          ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db     93 GGTGGGAGTCTGGGGGAGGGCCTGGTCAAGCCTGGGGGGTCCCTGAGGAGTCTCCTGCCAGC     152

Qy     84 CTCTGGGATTCACCTTCAGTAGGTAGTAGCCATGCACTGGGTCCGCCCAGGGGTCCAGGGAAGGG    143
          |||||||||||| ||||| |  |  ||| |||||||||||||||||| ||||||||||||||||
Db     93 CTCTGGGATTCACCTTCACCTTACCTTATACCATGAACTGGGTCCGCCCAGGCCTCCAGGGAAGGG   212

Qy    144 GCTGGGAGTGGGGTCTCATCCATTPAGTAATAGTAATACTTACATTATACTTACGAGACGGCAGT    203
          |||||||||||||||||||||||| |||| |  |  |||||||||||||||||||| | |||
Db    153 GCTGGGAGTGGGGTCTCATCCATGAGTAGTTACATTATACTTACGAGACTCAGT              272

Qy    204 GAAGGGCCGGATTCACCATCTCCAGAGAGACAAACGCCCAAGAAACTCACTGTTATCTGCAAATGAA    263
          |||||||||||||||||||||||||||||||||||||||||||||||||| |||||   ||| |
Db    213 GAAGGGCCGGATTCACCATCTCCAGAGAGACAAACGCCCAAGAAACTCACTGTATCTGCAGATGAA   332

Qy    264 CAGCCTGAGAGCCCAGCACACGGCTGTGTTACTTACTGTCGGAGAG          307
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Db    273 GAAGGGCCGATTCACCATCTCCAGAGACAACCGCCAAGAAACTCACTGTATCTGCAGATGAA

Qy    264 CAGCCTGAGAGCCCAGCACACGGCTGTGTTACTTACTGTGCGAGAG         307
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Db    333 CAGCCTGAGAGCCGAGGACACCGCTGTGTCTATTTACTTGTGCGAGAG        376
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Search completed: September 24, 2003, 04:42:48
Job time : 2285 secs

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: September 24, 2003, 02:57:23 ; Search time 67 Seconds
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Title: US-09-848-798A-97
Perfect score: 393
Sequence: 1 gaggtgcagctgctcgagtc..........ccacggtcatcgtctcctca 393

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum Match 0%
Maximum DB seq length: 0
Minimum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 60 summaries

Database :   Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	% Query Match	Length	DB	ID	Description
1	393	100.0	393	3	US-09-240-274-97	Sequence 97, Appl
2	363.6	92.5	381	3	US-09-240-274-96	Sequence 96, Appl
3	272.2	69.3	519	4	US-08-545-809A-23	Sequence 23, Appl
4	257.2	65.6	743	3	US-08-545-809A-48	Sequence 48, Appl
5	253.6	64.5	376	5	PCT-US93-12501-2	Sequence 2, Appl
6	248	63.1	747	4	US-10-039-785-65	Sequence 65, Appl
7	245.8	62.5	715	3	US-08-545-809A-11	Sequence 11, Appl
8	244.2	62.1	381	3	US-09-240-274-182	Sequence 182, App
9	243.6	62.0	378	3	US-09-240-274-195	Sequence 195, App
10	242	61.6	378	3	US-09-240-274-95	Sequence 95, Appl
11	240.4	61.2	369	1	US-08-082-623-1	Sequence 1, Appl
12	238.8	60.8	378	3	US-09-240-274-94	Sequence 94, Appl
13	238.8	60.8	378	4	US-09-240-274-196	Sequence 196, App
14	236.8	60.3	369	4	US-09-560-198A-1	Sequence 1, Appl
15	235.6	59.9	939	4	US-09-079-029-7	Sequence 7, Appli
16	234.2	59.6	354	2	US-08-652-816A-22	Sequence 22, Appl
17	234	59.5	387	3	US-09-000-088-3	Sequence 3, Appli
18	233.6	59.4	387	3	US-09-560-198A-3	Sequence 3, Appli
19	233.2	59.3	342	2	US-08-477-553A-51	Sequence 51, Appl
20	232.4	59.1	381	3	US-09-240-274-87	Sequence 87, Appl
21	232.4	59.1	375	3	US-09-240-274-88	Sequence 88, Appl
22	231.2	58.8	867	3	US-08-862-124-16	Sequence 16, Appl
23	231.2	58.8	867	3	US-08-862-124-13	Sequence 13, Appl
24	231.2	58.8	918	3	US-08-862-124-15	Sequence 15, Appl
c 25	231	58.8	918	3	US-08-862-124-18	Sequence 18, Appl
26	231	58.8	351	2	US-08-428-197-35	Sequence 35, Appl
27	231	58.8	351	5	PCT-US93-10555-35	Sequence 35, Appl
28	230.8	58.7	378	3	US-09-240-274-84	Sequence 84, Appl
29	230.6	58.7	514	3	US-08-545-809A-24	Sequence 24, Appl
30	230.6	58.7	877	3	US-08-545-809A-7	Sequence 7, Appli
31	230.4	58.6	369	4	US-09-560-198A-9	Sequence 9, Appli
32	230.2	58.6	378	3	US-09-240-274-82	Sequence 82, Appl
33	229.8	58.5	381	3	US-09-240-274-80	Sequence 80, Appl
34	229.8	58.5	512	3	US-08-545-809A-30	Sequence 30, Appl
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c 37	229.2	58.3	378	3	US-09-240-274-85	Sequence 85, Appl
38	229.2	58.3	378	3	US-09-240-274-189	Sequence 189, App
39	229	58.3	384	3	US-09-240-274-70	Sequence 70, Appl
40	228.4	58.1	342	2	US-08-477-553A-53	Sequence 53, Appl
41	228.2	58.1	5925	4	US-09-315-926A-78	Sequence 78, Appl
42	227.8	58.0	335	2	US-09-477-553A-55	Sequence 55, Appl
43	227.6	57.9	378	3	US-09-240-274-190	Sequence 190, App
44	227.4	57.9	384	3	US-09-240-274-185	Sequence 185, App
45	226.6	57.7	381	3	US-09-240-274-188	Sequence 188, App
46	226	57.5	378	3	US-09-240-274-86	Sequence 86, Appl
47	225.8	57.5	583	3	US-08-545-809A-33	Sequence 33, Appl
48	225.4	57.4	294	2	US-08-428-197-47	Sequence 47, Appl
49	225.4	57.4	294	5	PCT-US93-10555-47	Sequence 47, Appl
50	225.4	57.4	378	3	US-09-240-274-192	Sequence 192, App
51	224.8	57.2	369	2	US-08-428-197-37	Sequence 37, Appl
52	224.8	57.2	369	5	PCT-US93-10555-37	Sequence 37, Appl
53	224.4	57.2	375	3	US-09-240-274-89	Sequence 89, Appl
54	224.4	57.1	908	4	US-09-273-839A-9	Sequence 9, Appli
55	224	57.1	903	4	US-09-273-839A-12	Sequence 12, Appli
56	224	57.0	913	4	US-09-273-839A-10	Sequence 10, Appli
57	223.6	56.9	432	1	US-08-026-320A-1	Sequence 1, Appli
58	223.2	56.8	375	3	US-09-240-274-78	Sequence 78, Appl
59	223.2	56.8	375	3	US-09-240-274-90	Sequence 90, Appl
60	223.2	56.8	375	3	US-09-240-274-93	Sequence 93, Appl

ALIGNMENTS

RESULT 1
US-09-240-274-97

Sequence 97, Application US/09240274

Patent No. 6255455

GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 97
LENGTH: 393
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain E03
US-09-240-274-97

Query Match   100.0%; Score 393; DB 3; Length 393;
Best Local Similarity 100.0%;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GAGGTGCAGCTGCTCGAGTCTGGGGTGGAGTCTGGGGGAGGCCTGGTGCAAGCCTGGGGG 60
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RESULT 2
US-09-240-274-96
; Sequence 96, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09,240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 96
; LENGTH: 381
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain E01
US-09-240-274-96

  Query Match             92.5%;  Score 363.6;  DB 3;  Length 381;
  Best Local Similarity   98.9%;  Pred. No. 8.4e-104;
  Matches  366;  Conservative  0;  Mismatches  4;  Indels  0;  Gaps  0;

Qy          24 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
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Qy          84 CTCTGGATTCACCTTCAGTAGCTATAGCACATGGGGTCCGCGCCAGGGTCCCAGGGAAGG 143
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          72 CTCTGGATTCACCTTCAGTAGCTATAGCCATGCACTGGGGTCCGCCAGGCTCCAGGGAAGG 131

Qy         144 GCTGGAGTGGGGGTTCTCATCCATTAGTAATAGTAATAATAGTTACATTACACGCAGCGAGT 203
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         132 GCTGGAGTGGGTCTCATCCATTAGTAATAGTAATACTTACATTACACGCAGCGAGT 191

Qy         204 GAAGGGCCGATTCACCATCTCCAGAGACAGAGACTCACTGTATCTGCAAATGAA 263
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         192 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 251

Qy         264 CAGCCTGAGAGCCGAGCACACGCGCTGTGTGTACTACTGTGCGAGAGATACACAGTAA 323
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         252 CAGCCTGAGAGCCGAGGACACGCGGTGTGTTACTACTGTGCGAGAGATTCTAGATACACAGTAA 311

Qy         324 TTTCCTCCGTTGGGTTCGGACGACGGGTATGGACGTCTGGGGCCCCAAGGGACCACGGTCAT 383
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Db         300 GCTCGGAGTGGGTCTCATCCATTAGTAGTAGTAGTAGTTACATTATACTACGCAGACTCAGT 359
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```
RESULT 3
US-08-545-809A-21
; Sequence 21, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 10-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 27-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 519 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: human lymphoblast
; CELL LINE: CGM1
US-08-545-809A-21

  Query Match             69.3%;  Score 272.2;  DB 3;  Length 519;
  Best Local Similarity   97.2%;  Pred. No. 2.6e-75;
  Matches  277;  Conservative  0;  Mismatches  8;  Indels  0;  Gaps  0;

Qy          24 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         312 TTTCCTCCGTTGGGTTCGGACGACGGGTATGGACGTCTGGGGCCCAAGGGACCACGGTCAT 371

Qy          84 CTCTGGATTCACCTTCAGTAGCTATAGCGATAGCATGCACTGGGGTCCGCGCCAGGGTCCAGGGAAGGG 143
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         180 GGTGGAGTGGGTCTCATCCATTAGTAGTAGTAGTAGTTACATTATACTACGCAGACTCAGT 239

Qy         144 GCTGGAGTGGGTGTCATCCATTAGTAATAGTAATAATACTTACATTACACGCAGACTCAGT 203
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         240 CTCTGGATTCACCTTCAGTAGCTATAGCGATAGCATGCACTGGGGTCCGCGCCAGGGTCCAGGGAAGGG 299

Qy         204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         300 GCTGGAGTGGGTCTCATCCATTAGTAGTAGTAGTAGTTACATTATACTACGCAGACTCAGT 359
```

Qy   204 GAAGGGCCGATTCACCATCTCCAGAGAGACAACCGCCAAGAACTCACTGTATCTGCAAATGAA 263
         ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db   360 GAAGGGCCGATTCACCATCTCCAGAGACAACCGCCAAGAACTCACTGTATCTGCAAATGAA 419

Qy   264 CAGCCTGAGAGCCGAGGACACACGGCCGTGTGTACTACTGTGCGAGAGA 308
         ||||||||||||||||||||||||||| |||| |||||||||||||||
Db   420 CAGCCTGAGAGCCGAGGACACACGGCCGCTGTGTATTACTGTGCGAGAGA 464

RESULT 4
US-08-545-809A-48
; Sequence 48, Application US/0854580A
; Patent No. 6096878
; GENERAL INFORMATION:
;   APPLICANT: Honjo, Tasuku
;   APPLICANT: Matsuda, Fumihiko
;   TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
;   TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
;   NUMBER OF SEQUENCES: 145
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Fish & Richardson, P.C.
;   STREET: 225 Franklin Street
;   CITY: Boston
;   STATE: MA
;   COUNTRY: US
;   ZIP: 02110-2804
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: Windows95
;   SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/545,809A
;   FILING DATE: 27-MAR-1996
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/JP93/00603
;   FILING DATE: 10-MAY-1993
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Freeman, John W.
;   REGISTRATION NUMBER: 29,066
;   REFERENCE/DOCKET NUMBER: 06501/004001
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 617-542-5070
;   TELEFAX: 617-542-8906
;   TELEX: 200154
; INFORMATION FOR SEQ ID NO: 48:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 743 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: Genomic DNA
;   ORIGINAL SOURCE:
;   ORGANISM: Homo sapiens
;   CELL TYPE: human lymphoblast
;   CELL LINE: CGM1
US-08-545-809A-48

Query Match   65.6%; Score 257.8; DB 3; Length 743;
Best Local Similarity   94.0%; Pred. No. 9e-71;
Matches 268; Conservative   0; Mismatches 17; Indels   0; Gaps   0;

Qy   24 GGTGGAGTCTGGGGGAGGCGTGGTCAAGCCTGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
         ||||||||||||||||||| |||||| ||||||||| |||||||||||||||||||||||
Db   345 GGTGGAGTCTGGGGGAGGCTTGGTCACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 404

Qy   84 CTCTGGATTCACCTTCAGTAGCTATAGCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGG 143
         |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db   405 CTCTGGATTCACCTTCAGTAGCTATAGCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGG 464

Qy   144 GCTGGAGTGGGTCTCATCCATTAGTAGTAATAACTTAACATATACGCACGACGCAGT 203
         |||||||||||| ||| |||||||| ||||| || | |||||||| || ||
Db   465 GCTGGAGTGGGTTTCATACATTAGTAGTAGTACCATATACTACGCAGACTCTGT 524

Qy   204 GAAGGGCCGATTCACCATCTCCAGAGAGACAACCGCCAAGAACTCACTGTATCTGCAAATGAA 263
         ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   525 GAAGGGCCGATTCACCATCTCCAGAGACAACCGCCAAGAACTCACTGTATCTGCAAATGAA 584

Qy   264 CAGCCTGAGAGCCGAGGACACACGGCCGTGTGTACTACTGTGCGAGAGA 308
         ||||||||||||||||||||||||||| |||| ||||||||||||||||
Db   585 CAGCCTGAGAGCCGAGGACACACGGCCGCTGTGTATTACTGTGCGAGAGA 629

RESULT 5
PCT-US93-12501-2
; Sequence 2, Application PC/TUS9312501
; GENERAL INFORMATION:
;   APPLICANT: Chang, Tse Wen
;   TITLE OF INVENTION: ALLERGEN-SPECIFIC IgA MONOCLONAL ANTIBODIES AND
;   TITLE OF INVENTION: RELATED PRODUCTS FOR ALLERGY TREATMENT
;   NUMBER OF SEQUENCES: 10
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US93/12501
;   FILING DATE:
;   CLASSIFICATION:
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Tanox Biosystems, Inc.
;   STREET: 10301 Stella Link Rd.
;   CITY: Houston
;   STATE: Texas
;   COUNTRY: USA
;   ZIP: 77025
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5" Hi Density Diskette
;   COMPUTER: IBM PS/2
;   OPERATING SYSTEM: DOS, Version 3.30
;   SOFTWARE: Wordperfect 5.1
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Mirabel, Eric P.
;   REGISTRATION NUMBER: 31,211
;   REFERENCE/DOCKET NUMBER: TNX92-3
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 713-664-2288
;   TELEFAX: 713-664-8914
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 376 nucleotides
;   TYPE: nucleic acid
;   STRANDEDNESS: double stranded
;   TOPOLOGY: Linear
PCT-US93-12501-2

Query Match   64.5%; Score 253.6; DB 5; Length 376;
Best Local Similarity   81.5%; Pred. No. 1.4e-69;
Matches 308; Conservative   0; Mismatches 64; Indels   6; Gaps   1;

Qy   16 GAGTCTGGGGGTGGAGTCTGGGGGAGGCGTCAAGCCTGGGGGGTCCCTGAGACTCTCC 75
         ||| || |||||||||||||||||| ||||||||||||||||||||||||||||
Db   4 GAGCAGGTGGTGGAGTCTGGGGGAGGCCAGTCAAGCCTGGGGGGTCCCTGAGACTCTCC 63

Qy   76 TGTGCAGCCTCTGGATTCACCTTCAGTAGCTATAGCATACCATTAGTGT 135
         |||||||||||||||||||| | ||||| ||||| |||||||||||||
Db   64 TGTGCAGCCTCTGGATTCAATTCACCAGCTATACAGCATTAGTGT 135

Qy   136 GGGAAGGGGCTGGAGTGGGTCTCATCCATCCATTAGTAGTAATACAGTAT 195
         ||||| ||| ||||||||||||| ||| |||||| |||||||||||||
Db   124 GGGAAGGGGCTGGAGTGGGTCGCATCCAATTACGACGAGAAGTACTTACACCTTCACGGCA 183

Qy   196 GACGGCAGTGAAGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 255
         ||||||| | || ||| |||||||||||| | | |||| ||||| ||||||| || |||
Db   184 GACTCATTGAAGGGCGGGTTCACCATCTCCAGAGACAACGCCAAGAACTCTCTGTATCTG 243

Qy   256 CAAATGAACAAGCCTGAGAGCCGCAGACACGGCACACGGCGCTGTGTACTACTGTGCGAGAGATTCTAGA 315
         ||| ||||| |||||||||||| |||||||| ||||||||||||||||||||| ||| ||||| ||||
Db   256 CAAATGAACAAGCCTGAGAGCCGCAGACACGGCACACGGCGCTGTGTACTACTGTGCGAGAGATTCTAGA 315

```
Db  244 CAAATGAACAGCCCTGAGAGCCGAGGACCACCGGCTGTGTTATTACTGTGCCGAGAG------TA 297
        ||| | | | ||||||||||||| |||||||||||||| ||||| || ||||||||||    |
Qy  316 TACACGTAATTTTCCTCCGTTGGGTTCGGACGGACCGGTATGGACGTCTGGGGCCAAGGGACC 375
                                        || |   ||||||||| |||||| ||||||||
Db  298 TTGATCTTTGACTCAAACAAACTTTTATTACTACTACATGGACGGTCTGGGGGCCAAAGGGACC 357
                                                                           |||||| ||||||||
Qy  376 ACGGTCATCGTCTCCTCA 393
        ||||||   |||||||||
Db  358 ACGGTCGCCGTCTCCTCA 375
```

RESULT 6
US-10-039-785-65
; Sequence 65, Application US/1003785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 747
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding T1006F07 scFv
US-10-039-785-65

Query Match   63.1%; Score 248; DB 4; Length 747;
Best Local Similarity   82.0%; Pred. No. 1e-67;
Matches 300; Conservative   0; Mismatches 60; Indels   6; Gaps   1;

```
Qy   24 GGTGGAGTCTGGGGGAGGGCCTGGTCAAGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
         |||||||||||||| |||||||||||||||||||||||| |||||||||||||||||||||
Db   12 GTTTGGAGTCTGGGGGAGGGCTTGGGTACAGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAC 71
Qy   84 CTCTGGATTCACCTTCAGTAGCTATTAGCACTGGGTCCGGCCAGGGTCCAGGGAAGGG 143
         ||||||||||||| ||| ||||| |||||| |||||||||||||||||||||||||||
Db   72 CTCTGGATTCACCTTAGCAGCTATGCCATGAGCTGGGTCCGCCCAGGGTCCAGGGAAGGG 131
Qy  144 GCTGGAGTGGGTCTCATCCATTAATAGTAATAATACTTACATATTACTACGCCACAGCAGT 203
         ||||||||||||||||| || | ||| ||||||||||| ||||||| |||| || |||||
Db  132 GCTGGAGTGGGTTCAGCTATTAGTGGTAGTGGGTAGCACATATACTACGCCACAGCAGT 191
Qy  204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
         |||||||||||||||||||||||||||||| ||||| |||| |||| |||||| || ||
Db  192 GAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACCGTGTATCTGCAAATGAA 251
Qy  264 CAGCCTGAGAGCCGAGACACACGGGCTGTGTACTACTGTGCCGGAGAGATTCTAGATATACAGTAA 323
         |||||||||||||||||| ||||| ||||||||||||||| ||||| || ||  |||| |
Db  264 CAGCCTGAGAGCCGAGACACGCGGGCTGTGTACTGCTGGGGGTCTCATCCATTAGTAATAGTAATAGTAATACTTAC 183
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RESULT 7
US-08-545-809A-11
; Sequence 11, Application US/0854580 9A
; Patent No. 6096678
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 10-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 27-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 715 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: human lymphoblast
; CELL LINE: CGM1
US-08-545-809A-11

Query Match   62.5%; Score 245.8; DB 3; Length 715;
Best Local Similarity   87.9%; Pred. No. 4.8e-67;
Matches 268; Conservative   0; Mismatches 37; Indels   0; Gaps   0;

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Qy    4 GTGCAGCTGCTCGAGTCTGGGGGTGGAGTCTGGGGGAGGGCCTGGTCAAGCCTGGGGGGGTCC 63
        |||  | ||  ||||||| |||||||  |||| |  ||||||||||  |  ||||||| ||
Db  351 GTCCAGTGTCAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCC 410
Qy   64 CTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCACTAGCTATATAGCCACTGGGTC 123
        |||||||||||||||||||| ||||||||||| ||| | | |||| || |||||||||
Db  411 CTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTGACTACTACATGAGCTGGATC 470
Qy  124 CGCCAGGGGTCCAGGGAAGGGGCTGGAGTGGGTGGAGTGGGTGTCATCCATTAGTAATAGTAATAGTAATACTTAC 183
```

Db 471 CGGCCAGGCGTCCAGGGAAGGGGGCTGGAGTCGGGTTTCATACATTAGTAGTTAGTAGTACC 530

Qy 184 ATATACTACGCACAGACGCAGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAAC 243
Db 531 ATATACTACGCACAGACTCTGTGAAGGGCCGATTCACCATCTCCAGGGACAACGCCAAGAAC 590

Qy 244 TCACTGTATCTGCAAAATGAACAGGCCGACACACGGCGTGTGTACTACTGTGCG 303
Db 591 TCACTGTATCTGCAAAATGAACAGCCTGAGAGCCGAGGACACGGGCGTGTATTACTGTGCG 650

Qy 304 AGAGA 308
Db 651 AGAGA 655

RESULT 8
US-09-240-274-182
Sequence 182, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 182
; LENGTH: 381
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH10
US-09-240-274-182

Query Match   62.1%;   Score 244.2;   DB 3;   Length 381;
Best Local Similarity   80.8%;   Pred. No. 1.2e-66;
Matches   298;   Conservative   0;   Mismatches   68;   Indels   3;   Gaps   1;

Qy 25 GTGGAGTCTGGGGGAGGCCTGGGGGGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCC 84
Db 16 GAGGAGTCTGGGGGAGGCGTGGTCCAGCGTCCAGCCTGGGGGGTCCCTGAGACTTCCTGTGCAGCG 75

Qy 85 TCTGGATTCACCTTCAGTAGCTATAGCACATGCACTGGGTCCGCCAGGGTCCAGGGAAGGGG 144
Db 76 TCTGGGTTCACCTTCAGTAGGCATCACTGGGTCCGCCAGGCTCCTGGCAAGGG 135

Qy 145 CTGGAGTGGGTGTCTCATCCATTAGTAATAGTTACATATAATACGCCAGACGACGCAGT 204
Db 136 CTGGAGTGGGTGGCATTTATAATGGTTTGAGGTAATAATTACTATATCCAGACTCCGTG 195

Qy 205 AAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGTATCTGCAAATGAAC 264
Db 196 AAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACACGCCTGTATCTGTATCTGCAAATGAAC 255

Qy 265 AGCCTGAGAGCCGAGGACACGGGCGTGTGTACTACTGTGCGAGAGATTCTAGATACAGTAT 324
Db 256 AGCCTGAGAGCCGAGGACACGGCGTTGTGTPATTACTGTGCGAGAGAGGAGCTCTGTTTCCG 315

Qy 325 TTCCTCCGTTGGGGTTCGGAGCGACGGTATGGAACGTCTGGGGCCAAGGGACCACGGTCATC 384
Db 316 GGACTTACTCGG---TGGTCCTACGGCATGGACGCTCTCTGGGGCCAAGGGACCACGGTCAGC 372

Qy 385 GTCTCCCTCA 393
Db 373 GTCTCCCTCA 381

RESULT 9
US-09-240-274-195
Sequence 195, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 195
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-240-274-195

Query Match   62.0%;   Score 243.6;   DB 3;   Length 378;
Best Local Similarity   80.5%;   Pred. No. 1.8e-66;
Matches   298;   Conservative   0;   Mismatches   69;   Indels   3;   Gaps   1;

Qy 24 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
Db 12 GCTCGAGTCGGGGGAGGCGTGGTCCAGCGTCCAGCCTGGGGGGTCCCTGAGACTTCCTGTGCAGC 71

Qy 84 CTCTGGATTCACCTTCAGTAGCTATAGCACATGCACTGGGTCCGCCAGGGTCCAGGGAAGGGG 143
Db 72 GTCTGGGTTCACCTTCAGTAGGCATCACTGGGTCCGCCAGGCTCCTGGCAAGGG 131

Qy 144 GCTGGAGTGGGTGTCTCATCCATTAGTAATAGTTACATATAATACGCCAGACGACGCAGT 203
Db 132 GCTGGAGTGGGTGGCATTTATAATGGTTTGAGGTAATAATTACTATATCCAGACTCCGT 191

Qy 204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGTATCTGCAAATGAA 263
Db 192 GAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACACGCCTGTATCTGTATCTGCAAATGAA 251

Qy 264 CAGCCTGAGAGCCGACGACACGGGCGTGTGTACTACTGTGCGAGAGATTCTAGATACAGTAA 323
Db 252 CAGCCTGAGAGCCGAGGACACGGCGTTGTTATTACTGTGCGAGAGAGGAGCTCTGTTTTCG 311

Qy 324 TTTCCTCCGTTGGGGTTCGGAGCGACGGTATGGGACGTCTGGGGCCAAGGGGACCACGGTCAT 383
Db 312 GGGACTTACTCGG---TGGTCCTACGGCATGGACGCGTCTCTGGGGCCAAGGGACCACGGTCAG 368

Qy 384 CGTCTCCCTCA 393
Db 369 CGTCTCCCTCA 378

RESULT 10
US-09-240-274-95
Sequence 95, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550

NAME: Smith, Willaim M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-055-1
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (415) 326-2400
  TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 1:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 369 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  MOLECULE TYPE: DNA (genomic)
  ORIGINAL SOURCE:
    ORGANISM: Homo sapiens
  FEATURE:
    NAME/KEY: misc_feature
    LOCATION: 1..369
    OTHER INFORMATION: /standard_name= "Nucleotide
    OTHER INFORMATION: Sequence of the v-h region of SDZ MSL 109"
US-08-082-623-1
Patent No. 5750106

Query Match   61.2%;   Score 240.4;   DB 1;   Length 369;
Best Local Similarity 80.9%;   Pred. No. 1.8e-65;
Matches 296;   Conservative 0;   Mismatches 61;   Indels 9;   Gaps 1;

```
Qy  16 GAGGTCTGGGGGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCC  75
        |||  | || || ||||||  |||||||||||||||||||||||| ||||||||||||||||
Db   4 GAGCAAGTGCTGGAAATCTGGGGAGGCCTGGTCAAGCCTGGGAGGTCCCTGAGACTCTCC  63

Qy  76 TGTGCAGCCTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGGTCCA 135
        |||||||||||||| |||||||||||   ||||||| ||| ||||||||||||||| ||||
Db  64 TGTGCAGCCTCTGGTTTCACCTTCAGTCCCTATAGCGTCTTTTGGGTCCGCCAGGCTCCA 123

Qy 136 GGGAAGGGGCTGGAGTGGGTCTCATCCATTAATAGTAGTAATACTTACATATATACTACGCA 195
        || |||| || ||||||||||||||||||||||||||| ||||||| ||||| |||| |||
Db 124 GGAAGAGGGCCTGGAGTGGGTCTCATCCATTAATAGTACTTACAAATATTACCGCA 183

Qy 196 GACGCAGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 255
        |||  ||||||||||||| ||||||||||||||||||||||| |||||||| | | ||||
Db 184 GACTCAGTGAAGGGCCGCTTCACCATCTCCAGAGACAACGCCGAGAACTCAATATTTCTG 243

Qy 256 CAAATGAACAACCCTGAGAGCCGAGACACACGGCTGTGTACTACTGTGCGAGAGATTCTAGA 315
        |||||||||| |||||||||||||||| || |||||| | |||||||||||||||||||| |
Db 244 CAAATGAACAGCCTGAGAGCCGAGACACGGCTGTTTATTACTGTGCGAGAGATTCTGA 303

Qy 316 TACAGTAATTCCTCCGT------TGGGTTCGGGACGAGACGGTATGGGGCCCA 366
        || | | |  | ||||       | |||| || ||| | |||| ||||| | |||
Db 304 TATTACGCGTTTTTCGGAGTGGTTCTTTGTCGGACTACTACGGTCTGGGACGTCTGGGGC 363

Qy 367 CAAGGG 372
        ||||||
Db 364 CAAGGG 369
```

RESULT 12
US-09-240-274-94
Sequence 94, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0

EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 95
  TYPE: DNA
  LENGTH: 378
  ORGANISM: Homo sapiens
  FEATURE:
  OTHER INFORMATION: anti-Rh(D) chain D31
US-09-240-274-95

Query Match   61.6%;   Score 242;   DB 3;   Length 378;
Best Local Similarity 80.3%;   Pred. No. 5.7e-66;
Matches 297;   Conservative 0;   Mismatches 70;   Indels 3;   Gaps 1;

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Qy  24 GGTGGAGGTCGGGGGGAGGCCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGCAGC  83
        | |  || ||||||||||||  ||||||||||||||||| |||||||||||||||| ||||
Db  12 GCTCCAGTCGGGGGGAGGCGGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGC  71

Qy  84 CTCTGGATTCACCTTCAGTAGCTATTAGCATTCACTGGGTCCGCCAGGGTCCAGGGAAGGG 143
        | |||||||||||||||||||||||   | || |||||||| |||||| ||||| ||||||
Db  72 GTCTGGATTCACCTTCAGTAGCTATGGCACTGGGTCCGGCCAGGCTCCAGGCAAGGG 131

Qy 144 GCTGGAGTGGGTCTCATCCATTAGTAAATAGTAATACTTACATATATACTACGACGCCAGT 203
        |||||||||||| ||||||||||||||| ||||||| |||||||| |||||||| || |||
Db 132 GCTGGAGTGGGTGGCAGTGTCTACTATGATTGGGAAGTAACAAACACTATTCAGACTCCGT 191

Qy 204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATGTCCAAATGAA 263
        ||||||||||||||||||||||| |||||||||| | | |||| ||||| | |||| |||
Db 192 GAAGGGCCGATTCACCATCTCCAAGAACACAGCGTCGTATCTACAAATGGA 251

Qy 264 CAGCCTGAGAGCCGAGGACACGGCTGTGTACTACTGTGCGAGAGATTCTTAGATACAGTAA 323
        |||||||||||||||||||||||||||||| |||||||||||||||   | |  ||||| |
Db 252 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGA---AAGAAATTTTCG 308

Qy 324 TTTCCTCCGGTTGGGGTTCGGGACGAGACGGTATGGGGGCCAAGGGACCACGGTCAT 383
        | || | |  | |||| | |||| ||| ||||||| |||||| ||||||||||||| |
Db 309 GAGTGGTTATTCCCGCTACTACGGTATGGACGTCTGGGGCCCAGGGACCACGGTCAC 368

Qy 384 CGTCTCCTCA 393
        ||||||||||
Db 369 CGTCTCCTCA 378
```

RESULT 11
US-08-082-623-1
Sequence 1, Application US/08082623
Patent No. 5750106
GENERAL INFORMATION:
APPLICANT: Ostberg, Lars G.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO
TITLE OF INVENTION: CYTOMEGALOVIRUS
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/082,623
  FILING DATE: 25-JUN-1993
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 435
  CLASSIFICATION:
  FILING DATE: 28-JAN-1993
APPLICATION NUMBER: US 08/010,228
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Townsend and Townsend Khourie and Crew
  STREET: 379 Lytton Avenue
  CITY: Palo Alto
  STATE: California
  COUNTRY: US
  ZIP: 94301
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: Patentin Release #1.0, Version #1.25
ATTORNEY/AGENT INFORMATION:

; SEQ ID NO 94
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D30
US-09-240-274-94

Query Match   60.8%;   Score 238.8; DB 3; Length 378;
Best Local Similarity 79.7%;   Pred. No. 5.6e-65;
Matches 295; Conservative 0; Mismatches 72; Indels 3; Gaps 1;

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Qy   24 GGTGGAGTCTGGGGGAGGCGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
         | |||| |||||| ||||||| |||||||||| |||||| ||||||||||||||||||||||
Db   12 GCTCGAGTCGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGC 71

Qy   84 CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGGTCCAGGGAAGG 143
         ||||||||||||||||||||||| ||| |||| |||||||||||||||||||||| |||
Db   72 GTCTGGATTCACCTTCAGTAGCTATGGCATGCCCTGGGTCCGCCAGGGTCCAGGCAAGGG 131

Qy  144 GCTGGAGTGGGTCTCATCCATTAGTAATAGTAATAATACATTATATACGCAGACGCAGT 203
         ||||||||||| | |  | ||||||  || |  | ||    |||| |||  |||| |||
Db  132 GCTGGAGTGGGTGGCAGTTGTCTACTATGGTGAAGTAACAAACACTATTCAGACTCCGT 191

Qy  204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
         |||||||||||||||||||||||||||||||||||||||||||||| | ||||  |||
Db  192 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCAGAGACACGGCTGTGTATTACTGTGCCGAGAGA 251

Qy  264 CAGCCTGAGAGCCGAGCACACGGCTGTGTCTACTACTGTGCGAGAGATTCTAGATACAGTAA 323
         ||||||||||||||| ||||||||||||| |||||||||||  |||||      ||| |
Db  252 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCCGAGAGA---AAGAAATTTTCG 308

Qy  324 TTTCCCTCCGTTGGGGTTCGGACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCAT 383
                 ||       | ||||||||||||||||||||||||  |||||||||||||||
Db  309 GAGTGGTTATTCCCGCTACTACTACGGTATGGACGTCTGGGGCCCAGGGACCACGGTCAC 368

Qy  384 CGTCTCCTCA 393
         ||||||||||
Db  369 CGTCTCCTCA 378
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RESULT 13
US-09-240-274-196
Sequence 196, Application US/09240274
Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09,240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 196
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH56
US-09-240-274-196

Query Match   60.8%;   Score 238.8; DB 3; Length 378;
Best Local Similarity 79.7%;   Pred. No. 5.6e-65;
Matches 295; Conservative 0; Mismatches 72; Indels 3; Gaps 1;

RESULT 14
US-09-560-198A-1
Sequence 1, Application US/09560198A
Patent No. 6492497
; GENERAL INFORMATION:
; APPLICANT: Thompson, Julia E
; APPLICANT: Lennard, Simon N
; APPLICANT: Wilton, Alison J
; APPLICANT: Braddock, Peta SH
; APPLICANT: Du Fou, Sarah L
; APPLICANT: McCafferty, John G
; APPLICANT: Conroy, Louise A
; APPLICANT: Tempest, Philip R
; TITLE OF INVENTION: Specific binding members for TGFbeta1
; FILE REFERENCE: 28111/35620A
; CURRENT APPLICATION NUMBER: US/09/560,198A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/131,983
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-560-198A-1

Query Match   60.3%;   Score 236.8; DB 4; Length 369;
Best Local Similarity 80.0%;   Pred. No. 2.3e-64;
Matches 296; Conservative 0; Mismatches 62; Indels 12; Gaps 1;

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Qy   24 GGTGGAGTCTGGGGGAGGCGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
         || ||  |||||| |||||| |||||||||||| ||||| |||||||||||||||||||||
Db   12 GGTGCAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGAGGTCCCTGAGACTCTCCTGTGCAGC 71

Qy   84 CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGGTCCAGGGAAGG 143
         |||||||||||||||| ||||||| |||| | ||||||||||||||||||||| ||||
Db   72 CTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGGTCCAGGCAAGGG 131

Qy  144 GCTGGAGTGGGTCTCATCCATTAGTAATAGTAATAATACATTATATACGCAGACGCAGT 203
         ||||||||||| | | | |||||| | |  | |  |  | |||||||||  |||| |||
Db  132 GCTGGAGTGGGTTGCAGTTATCATAGTAATAGTAAGTAACTACTACGCAGACTCCGT 191

Qy  204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
         |||||||||||||||||||||| |||||||||| ||||||| |||||||||||  |||||
Db  192 GAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAA 251

Qy  264 CAGCCTGAGAGCCGAGCACACGGCTGTGTCTACTACTGTGCGAGAGATTCTAGATACAGTAA 323
         ||||||||||||||| |||||||||||||||||||||||  |||||      |||| |
Db  252 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCCGAGAGA---AAGAAATTTTCG 308

Qy  324 TTTCCCTCCGTTGGGGTTCGGACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCAT 383
                 ||        |||||||||||||||||||||||||| |||||||||||||||
Db  309 GAGTGGTTATTCCCGCTACTACTACGGTATGGACGTCTGGGGCCCAGGGACCACGGTCAC 368

Qy  384 CGTCTCCTCA 393
         ||||||||||
Db  369 CGTCTCCTCA 378
```

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Qy  264 CAGCCTGAGAGCCGAGACACACGGCTGTGTACTACTGTGCGAGAGATTCTAGATACAGTAA 323
         |||||||||||| ||||||||||||||||||| ||||||||||||||  ||   |  | ||
Db  252 CAGCCTGAGAGCTGAGACACACGGCTGTGTATTACTGTGCGAGAGATATATAGTGG     311

Qy  324 TTTCCTCCGTTGGGTTCGGAGGGACGGGCCCAAGGGACCACGGTCAT 383
            |||-|
Db  312 CTAC--------GATACGAGTGGTGTGGAGCTCTGGGGGCAAGGGACCACGGTCAC 359

Qy  384 CGTCTCCCTCA 393
         |||||||| ||
Db  360 CGTCTCCTCA 369
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RESULT 15
US-09-079-029-7
Sequence 7, Application US/09079029
Patent No. 6342369
GENERAL INFORMATION:
  APPLICANT: Adams, Camilla W.
  APPLICANT: Ashkenazi, Avi J.
  APPLICANT: Chuntharapai, Anan
  APPLICANT: Kim, Kyung J.
  TITLE OF INVENTION: Apo-2 Receptor
  NUMBER OF SEQUENCES: 14
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: Genentech, Inc.
  STREET: 1 DNA Way
  CITY: South San Francisco
  STATE: California
  COUNTRY: USA
  ZIP: 94080
  COMPUTER READABLE FORM:
  MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: WinPatin (Genentech)
  CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/079,029
  FILING DATE:
  CLASSIFICATION:
  ATTORNEY/AGENT INFORMATION:
  NAME: Marschang, Diane L.
  REGISTRATION NUMBER: 35,600
  REFERENCE/DOCKET NUMBER: P1101R2
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: 650/225-5416
  TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 7:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 939 base pairs
  TYPE: Nucleic Acid
  STRANDEDNESS: Single
  TOPOLOGY: Linear
US-09-079-029-7

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Query Match            59.9%;   Score 235.6;   DB 4;   Length 939;
Best Local Similarity  80.1%;
Matches  293;  Conservative  0;  Mismatches  64;  Indels  9;  Gaps  1;
                                 Pred No. 8e-64;
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Qy   24 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
         ||||||||||||||||||| ||||| |||||||||||||||||||||||||||||||||
Db  129 GGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAC 188

Qy   84 CTCTGGATTCACCCTCAGTAGCTATAGCACTGGGTCCGCCAGGCTCCAGGGAAGG 143
         ||-||||||||||| |||||||||| |||||||||||||||||||||||||
Db  189 CTCTGGATTCACCCTTTAGTAGCTATTGGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGG 248

Qy  144 GCTGGAGTGGGTGTCTCATCCATTAGTAATAATAATACTTACATATATACTACCCAGACGCAGT 203
         |||||||||||  ||||  |||||            ||
Db  249 GCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAAATACTACTGTGGACTCTGT 308

Qy  204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  309 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 368

Qy  264 CAGCCTGAGAGCCGAGACACACGGCTGTGTACTACTGTGCGAGAGATTCTAGATACAGTAA 323
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  369 CAGCCTGAGAGCCGAGACACACGGCTGTGTACTACTGTGCGAGAGATTCTAGATACAGTAA 428

Qy  324 TTTCCTCCGTTGGGTTCGGAGGGACGGGCCCAAGGGACCACGGTCAT 383
          ||      |||   ||| |  |||  |||||||||||||||||
Db  429 GGGGCAGCTCGTCTGGGGTGG--------TTCGACCCCTGGGGGGAGAGGAGGACCACGGTCAC 479

Qy  384 CGTCTC 389
         |||||
Db  480 CGTTCTC 485
```

RESULT 16
US-08-652-816A-22
Sequence 22, Application US/08652816A
Patent No. 5872215
GENERAL INFORMATION:
  APPLICANT: Osbourn, JK
  APPLICANT: Allen, DJ
  APPLICANT: McCafferty, JG
  TITLE OF INVENTION: Specific binding members, materials and
  TITLE OF INVENTION: methods.
  NUMBER OF SEQUENCES: 53
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
  STREET: 6300 Sears Tower, 233 South Wacker Drive
  CITY: Chicago
  STATE: Illinois
  COUNTRY: United States of America
  COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
  CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/652,816A
  FILING DATE: 23-MAY-1996
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: GB 9125579.4
  FILING DATE: 02-DEC-1991
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: GB 9125579.8
  FILING DATE: 02-DEC-1991
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: GB 9206318.9
  FILING DATE: 24-MAR-1992
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: GB 9206372.6
  FILING DATE: 23-SEP-1992
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: GB 9525004.9
  FILING DATE: 07-DEC-1995
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: GB 9610824.6
  FILING DATE: 23-MAY-1996
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: PCT/GB92/02240
  FILING DATE: 02-DEC-1992
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/244,597
  FILING DATE: 01-JUN-1994
  ATTORNEY/AGENT INFORMATION:
  NAME: David W. Clough
  REGISTRATION NUMBER: 36,107
  REFERENCE/DOCKET NUMBER: 28111/33308
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 22:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 354 base pairs

```
;    TYPE: nucleic acid
;    STRANDEDNESS: double
;    TOPOLOGY: linear
US-08-652-816A-22

Query Match            59.6%;   Score 234.2;   DB 2;   Length 354;
Best Local Similarity   88.5%;   Pred. No. 1.5e-63;
Matches  254;  Conservative   0;  Mismatches  33;  Indels   0;  Gaps   0;

Qy      24 GGTGGAGTCTGGGGGAGGCGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC  83
           |||||||| |||||||||||||||||||||| ||| |||  ||||| ||||||||||||||||
Db      12 GGTGGAGTCTCAGGGGAGGCGTTGGTCACGACTCCTGAGACTCTCCTGTGCAGC  71

Qy      84 CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTTCGCCAGGCTCCAGGGAAGGG  143
           ||||| ||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db      72 CTCTGGATTCACCTTTAGCAGCTATAGCCATGAGTGGGTTCGCCAGGCTCCAGGGAAGGG  131

Qy     144 GCTGGAGTGGGTCTCATCCATTAGTAATAGTAATACTTACATATATACCGAGACGCCAGT  203
           ||||||||||||||| ||||| ||||| ||||||  ||||||||||||| |||||||| ||
Db     132 GCTGGAGTGGGTCTCAGCTATTAGTGGTAGTTAGCACATACTTACGCGACTCCGT  191

Qy     204 GAAGGGCCGATTCACCATCTCCAGAGACAAGCCAAGAACTCACTGTATCTGCAAATGAA  263
           |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db     192 GAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAA  251

Qy     264 CAGCCTGAGAGCCGACGCACACGGCTGTGTATTACTACTGTGCGAGAGATT  310
           ||||||||||||| |||||||||||||||||||||||||||||||||||||
Db     252 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCCGAGAGCTT  298
```

RESULT 17

```
US-09-000-088-3
;   Sequence 3, Application US/09000088
;   Patent No. 6146629
;   GENERAL INFORMATION:
;   APPLICANT: DAGAN, Shlomo
;   TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST HEPATITIS B VIRUS
;   TITLE OF INVENTION: SURFACE ANTIGEN (HBVsAg)
;   FILE REFERENCE: DAGAN-1
;   CURRENT APPLICATION NUMBER: US/09/000,088
;   CURRENT FILING DATE: 1997-06-10
;   EARLIER APPLICATION NUMBER: PCT/IL97/00183
;   EARLIER APPLICATION FILING DATE: 1997-06-10
;   EARLIER APPLICATION NUMBER: IL96/118626
;   EARLIER APPLICATION FILING DATE: 1996-06-11
;   NUMBER OF SEQ ID NOS: 4
;   SOFTWARE: PatentIn Ver. 2.0
;
;   SEQ ID NO 3
;   LENGTH: 387
;   TYPE: DNA
;   ORGANISM: HUMAN
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(387)
US-09-000-088-3

Query Match            59.5%;   Score 234;   DB 3;   Length 387;
Best Local Similarity   78.5%;   Pred. No. 1.8e-63;
Matches  295;  Conservative   0;  Mismatches  75;  Indels   6;  Gaps   1;

Qy      24 GGTGGAGTCTGGGGGAGGCGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC  83
           |||||||| |||||||||||||||||||| |||||||  ||||| |||||||||||||||||
Db      12 GGTGGAGTCAGGGGAGGCGTCCGGGGCCTGGGTCCGGACTCTCCTGTGCAGC  71

Qy      84 CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTTCGCCAGGCTCCAGGGAAGGG  143
           ||||| ||||||||||  ||||||||| |  |||||||||| |||||||||||||||||
Db      72 CTCTGGATTCACTTTCAGTGACTATAGAAAAACTGGGTTCCGCCAGGCTCCAGGGAAGGG  131

Qy     144 GCTGGAGTGGGTCTCATCCATTAGTAATAGTAATACTTACATATATACCGAGACGCCAGT  203
           ||||||||||||||||  || |||||  |||| |||||  || ||| |||||||| ||
Db     132 ACTGGAGTGGGTTGGCAATTATTTCATATGATGGAAGAATTACACTATCATATAGAGACTCCGT  191

Qy     204 GAAGGGCCGATTCACCATCTCCAGAGACAAGCCAAGAACTCACTGTATCTGCAAATGAA  263
           ||||||||||||||| |||||||||||||| ||||||| |||||||| |||||||||||
Db     192 GAAGGGCCGATTCACCAGAGCCGTCGGGTTCCGCCAGGGTCCAGGGAAGGG  251

Qy     264 CAGCCTGAGAGCCGACGCACACGGCTGTGTATTACTACTGTGCGAGAGATT  310
           ||||||||||||| |||||||||||||||||||||| ||  || |||||||
Db     252 CAGCCTGAGAGCTGAGGACACGGCTGTGTTATTACTGTGCGAGAGGG  311
```

RESULT 18

```
US-09-560-198A-3
;   Sequence 3, Application US/09560198A
;   Patent No. 6492497
;   GENERAL INFORMATION:
;   APPLICANT: Thompson, Julia E
;   APPLICANT: Lennard, Simon N
;   APPLICANT: Wilton, Alison J
;   APPLICANT: Bradock, Peta SH
;   APPLICANT: Du Fou, Sarah L
;   APPLICANT: McCafferty, John G
;   APPLICANT: Conroy, Louise A
;   APPLICANT: Tempest, Philip R
;   TITLE OF INVENTION: Specific binding members for TGFbeta1
;   FILE REFERENCE: 28111/35620A
;   CURRENT APPLICATION NUMBER: US/09/560,198A
;   CURRENT FILING DATE: 2000-04-28
;   PRIOR APPLICATION NUMBER: US 60/131,983
;   PRIOR APPLICATION FILING DATE: 1999-04-30
;   NUMBER OF SEQ ID NOS: 25
;   SOFTWARE: PatentIn Ver. 2.1
;
;   SEQ ID NO 3
;   LENGTH: 369
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-560-198A-3

Query Match            59.4%;   Score 233.6;   DB 4;   Length 369;
Best Local Similarity   79.5%;   Pred. No. 2.3e-63;
Matches  294;  Conservative   0;  Mismatches  64;  Indels   12;  Gaps   1;

Qy      24 GGTGGAGTCTGGGGGAGGCGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC  83
           |||||||| |||||||||||||||||||| |||||||  |||||||||||||||||||||||
Db      12 GGTGGAGTCTCGGGGGAGGCGTCGGTCCAGCCTGGGGGAGGTCGTCCAGCCTGAGACTCTCCTGTGCAGC  71

Qy      84 CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTTCGCCAGGCTCCAGGGAAGGG  143
           ||||| ||||||||||  ||||| ||| || |||||||||||||||||||||||||||||
Db      72 CTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG  131

Qy     144 GCTGGAGTGGGTCTCATCCATTAGTAATAGTAATACTTACATATATACCGAGACGCCAGT  203
           |||||||||||||||  || ||||| ||||| | |||  || ||| |||||||| ||
Db     132 GCTGGAGTGGGTGGCAGTTATATCATGAGTGAAGTAGTATTAAATACTATGGAGACTCCGT  191

Qy     204 GAAGGGCCGATTCACCATCTCCAGAGACAAGCCAAGAACTCACTGTATCTGCAAATGAA  263
           ||||||||||||||| ||||||||||||| |||||||||||||||||||||||||||||
Db     192 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACACGCTGTATCTGCAAATGAA  251

Qy     264 CAGCCTGAGAGCCGACGCACACGGCTGTGTATTACTACTGTGCGAGAGATT  323
           ||||||||||||| ||||||||||||| |||||||||||| |||||| ||
Db     252 CAGCCTGAGAGCTGAGGACACGGCTGTGTGTATTACTGTGCGAGATAGTGG  311

Qy     324 TTTCCTTCCGTTGGGTTCGGAGCGACGGACGGTATGGACGGTCTCAGGGAGACCACGGTCAT  383
           ||||||||||||||||||||||  ||| | ||| ||| |||||||||| |||||||||||
Db     312 CTAC-------GATACGGACCCCAGTACTCCTCGGGGGCCAAGGGACCACGGTCAC  359

Qy     384 CGTCTCCTTCA  393
           ||||||||||
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RESULT 19
US-08-477-553A-51
Sequence 51, Application US/0847553A
Patent No. 5919910
GENERAL INFORMATION:
APPLICANT: HUGHES-JONES, Nevin C
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,553A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,034
FILING DATE: 23-JUNE-1992
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8925590.5
FILING DATE: 13-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 007330-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..342
OTHER INFORMATION: /note= "Nucleotides 1-381 corres'.
OTHER INFORMATION: to nucleotides 24-365 of Fig. 10/14. Nucleotides
US-08-477-553A-51
OTHER INFORMATION: 1-23 and 366-381 represent PCR primers."

Query Match   59.3%;   Score 233.2; DB 2; Length 342;
Best Local Similarity   80.1%;   Pred. No. 3e-63;
Matches   274; Conservative   0; Mismatches   68; Indels   0; Gaps   0;

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Qy   156 CTCATCCATTAGTAATAGTAATTACTTACATATACTACGAGACCGAGTGAAGGGCCGATT     215
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RESULT 20
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Sequence 87, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 87
LENGTH: 381
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain D13
US-09-240-274-87

Query Match   59.1%;   Score 232.4; DB 3; Length 381;
Best Local Similarity   76.8%;   Pred. No. 5.5e-63;
Matches   284; Conservative   0; Mismatches   86; Indels   0; Gaps   0;

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Qy   384 CGTCTCCTCA 393
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Search completed: September 24, 2003, 04:44:05
Job time : 69 secs

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: September 24, 2003, 04:04:44 ; Search time 1825 Seconds

Title: US-09-848-798a-97
Perfect score: 393
Sequence: 1 gaggtgcagctgctcgagtc..........ccacggtcatcgtctcctca 393

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 1678620 seqs, 1244745471 residues

Total number of hits satisfying chosen parameters: 3357240

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 60 summaries

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   16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
   17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

(without alignments)
536.093 Million cell updates/sec

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	393	100.0	393	11	US-09-848-798-97	Sequence 97, Appl
2	363.6	92.5	381	11	US-09-848-798-96	Sequence 96, Appl
3	272.2	69.3	311	9	US-09-864-761-31233	Sequence 31233, A
4	270.8	68.9	379	12	US-10-041-860-55	Sequence 55, Appl
5	269.6	68.6	348	14	US-10-091-300-23	Sequence 23, Appl
6	269.6	68.6	348	14	US-10-091-300-27	Sequence 27, Appl
7	268	68.2	348	14	US-10-091-300-30	Sequence 30, Appl
8	262.8	66.9	414	12	US-10-325-694-143	Sequence 143, App
9	261.2	66.5	379	12	US-10-041-860-59	Sequence 59, Appl
10	261.2	66.5	382	12	US-10-041-860-75	Sequence 75, Appl
11	259.2	66.0	1413	14	US-10-153-382-16	Sequence 16, Appl
12	258	65.6	379	12	US-10-041-860-67	Sequence 67, Appl
13	250.4	63.7	520	10	US-09-844-684-10	Sequence 10, Appl
14	250.4	63.7	520	14	US-10-040-244-10	Sequence 10, Appl
15	248.8	63.3	375	14	US-10-172-317-1	Sequence 1, Appl
16	248	63.1	407	11	US-09-918-995-16657	Sequence 16657, A
17	248			13	US-10-039-785-65	Sequence 65, Appl
18	247.6			13	US-09-964-824A-583	Sequence 583, App
19	247.6			10	US-09-954-456-1188	Sequence 1188, Ap
20	246.4			11	US-09-972-656-73	Sequence 73, Appl
21	245.6			12	US-09-949-039-1	Sequence 1, Appl
22	245.6			12	US-09-969-748C-1	Sequence 1, Appl
23	244.2			11	US-09-848-798-182	Sequence 182, App
24	244.2			12	US-09-848-798-125404	Sequence 125404,
25	244.2			11	US-10-027-632-125405	Sequence 125405,
26	243.6			11	US-09-848-798-195	Sequence 195, App
27	242			12	US-10-330-613-31	Sequence 31, Appl
28	242			12	US-10-330-530-31	Sequence 31, Appl
29	242			11	US-09-848-798-95	Sequence 95, Appl
30	239.6			11	US-09-844-684-14	Sequence 14, Appl
31	239.6			14	US-10-040-244-14	Sequence 14, Appl
32	239.2			12	US-09-848-798-94	Sequence 94, Appl
33	238.8			11	US-09-848-798-196	Sequence 196, App
34	238.8			11	US-10-066-895-25	Sequence 25, Appl
35	238.4			13	US-10-066-895-85	Sequence 85, Appl
36	238			10	US-09-844-684-12	Sequence 12, Appl
37	238			14	US-10-040-244-12	Sequence 12, Appl
38	237.2			9	US-09-811-737-7	Sequence 7, Appl
39	237.2			12	US-09-811-737-24	Sequence 24, Appl
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43	236.4			10	US-09-423-800-58	Sequence 58, Appli
44	236.4			11	US-10-337-981-58	Sequence 58, Appl
45	236.4			14	US-10-182-018-58	Sequence 58, Appl
46	236.4			14	US-10-169-003-58	Sequence 58, Appl
47	235.6			12	US-10-288-917-7	Sequence 7, Appl
48	235.6			13	US-10-052-799-7	Sequence 109, Appl
49	235.2			13	US-10-066-895-27	Sequence 7, Appl
50	234			14	US-09-859-053-35	Sequence 27, Appl
51	233.6			12	US-10-243-265-3	Sequence 35, Appl
52	233.4			12	US-10-225-108A-1	Sequence 1, Appli
53	233.4			13	US-09-848-832-1	Sequence 1, Appli
54	233.4			13	US-10-066-895-14	Sequence 14, Appli
55	233.2			11	US-09-972-656-67	Sequence 67, Appl
56	233			11	US-09-822-849A-109	Sequence 7, Appl
57	232.4			11	US-09-848-798-87	Sequence 88, Appl
58	232.4			11	US-09-848-798-88	Sequence 87, Appl
59	231.6			11	US-09-988-115A-52	Sequence 52, Appl
60	231.2			11	US-09-848-798-183	Sequence 183, App

ALIGNMENTS

RESULT 1
US-09-848-798-97
Sequence 97, Application US/09848798
Publication No. US20030040605A1

GENERAL INFORMATION:
 APPLICANT: Siegel, Donald L.
 TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
 TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
 FILE REFERENCE: 09596-4202
 CURRENT APPLICATION NUMBER: US/09/848,798
 CURRENT FILING DATE: 2001-05-04
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/848,798
 PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 09/240,274
 PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-01-29
 PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 60/028,550
 NUMBER OF SEQ ID NOS: 224
 PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 97
 LENGTH: 393
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: anti-Rh(D) chain E03
US-09-848-798-97

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Best Local Similarity  100.0%;   Pred. No. 6.2e-121;
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; Sequence 96, Application US09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 0959-4202
;  CURRENT APPLICATION NUMBER: US-09/848,798
;  CURRENT FILING DATE: 2001-05-04
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
;  PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 96
;  LENGTH: 381
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  OTHER INFORMATION: anti-Rh(D) chain E01
US-09-848-798-96

Query Match         98.9%;   Score 363.6;  DB 11;   Length 381;
Best Local Similarity   92.5%;   Pred. No. 4e-111;
Matches 366;   Conservative  0;   Mismatches  4;   Indels  0;   Gaps  0;

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Db  131 ...  203
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RESULT 3
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; Sequence 31233, Application US09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT: Rank, David R.
;  APPLICANT: Hanzel, David K.
;  APPLICANT: Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
;  TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US-09/864,761
;  CURRENT FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
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;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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Db  372 CGTCTCCTCA 381
Qy  384 CGTCTCCTCA 393
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Db  372 CGTCTCCTCA 381
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;     TYPE: DNA
;     ORGANISM: Homo sapiens
;     FEATURE:
;     OTHER INFORMATION: MAP TO AB019439.1
;     OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.42
;     OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.51
;     OTHER INFORMATION: EST HUMAN HIT: AW403220.1, EVALUE 0.00e+00
;     OTHER INFORMATION: NT HIT: L29155.1, EVALUE 0.00e+00
;     OTHER INFORMATION: SWISSPROT HIT: P01764, EVALUE 3.00e-43
US-09-864-761-31233

Query Match             69.3%;    Score 272.2;  DB 9;   Length 311;
Best Local Similarity   97.2%;    Pred. No. 1.2e-80;
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            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       83 CTCTGGATTCACCTTCAGTAGCTATAGCATGAACTGGGTCCGCCAGGCTCCAGGGAAGGG 142

Qy      144 GCTGGAGTGGGTCATCCATTAGTAATAGTAATAGTAATATACTTACATATATACTACGCAGACGCAGT 203
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      143 GCTGGAGTGGGTCTCATCCATTAGTAGTAGTTACATATNTACGCAGACTCAGT 202

Qy      204 GAAGGGCCGATTCACCAATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      203 GAAGGGCCGATTCACCAATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 262

Qy      264 CAGCCTGAGAGCCGAGGACACACGGCTGTGTTACTACTGTGCGAGAGA 308
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db      263 CAGCCTGAGAGCCGAGGACACACGGCTGTGTTACTACTGTGCGAGAGA 307


RESULT 4
US-10-041-860-55
; Sequence 55, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
;     APPLICANT: Corvalan, Jose R.F.
;     APPLICANT: Jia, Xiao-Chi
;     APPLICANT: Feng, Xiao
;     APPLICANT: Yang, Xiao-Dong
;     APPLICANT: Chen, Francine
;     APPLICANT: Gazit, Gadi
;     APPLICANT: Weber, Richard
;     APPLICANT: Bezabeh, Binyam
;     TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
;     TITLE OF INVENTION: THEREOF
;     FILE REFERENCE: ABGENIX.051A
;     CURRENT APPLICATION NUMBER: US/10/041,860
;     CURRENT FILING DATE: 2002-01-07
;     NUMBER OF SEQ ID NOS: 377
;     SOFTWARE: FastSEQ for Windows Version 4.0
;     SEQ ID NO 55
;     LENGTH: 379
;     TYPE: DNA
;     ORGANISM: homo sapiens
US-10-041-860-55

Query Match             68.9%;    Score 270.8;  DB 12;  Length 379;
Best Local Similarity   85.1%;    Pred. No. 3.8e-80;
Matches  315;  Conservative  0;  Mismatches  52;  Indels  3;  Gaps  1;

Qy       24 GGTGGAGTCTGGGGGAGGCCCTGGTCAAGCCTGGGGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
            |||||||||||||||||||||||||||||||||||||||
Db       12 GGTGGAGTCTGGGGGAGGCCCTGGTCAAGCCTGGGGGGGGTCCCTGAGACTCTCCTGTGCAGC 71

Qy       84 CTCTGGATTCACCTTCAGTAGCTATAGCATGGGGTCCCCCAGGGGGTCCAGGGAAGGG 143
            |||||||||||||||||||||||||||||||||||||||||||
Db       72 CTCTGGATTCAACTTCAGAAACTTATAACATGAACTGGGTCCGCCAGGCTCCAGGGAAGGG 131
```

```
Qy      144 GCTGGAGTGGGTCTCATCCATTAGTAATAGTAATAGTAATACTTACATATATACTACGCAGACGCAGT 203
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      132 GCTGGAGTGGGTCTCATCCATTAGTAGTAGTTACATATATACGCAGACTCAGT 191

Qy      204 GAAGGGCCGATTCACCAATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      192 GAAGGGCCGATTCACCAATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 251

Qy      264 CAGCCTGAGAGCCGAGGACACACGGCTGTGTTACTACTGTGCGAGAGA 323
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db      252 CAGCCTGAGAGCCGAGGACACACGGCTATATTACTACTGTGCGAGAGATTA---TGATTAC 308

Qy      324 TTTCCTCCGTTGGGGTTCGGAGGCAGCGGTATGGACGTCTGGGGCCAAAGGGACCACGGTCAT 383
            ||| |||| |||||
Db      309 GTTTGGGGGAATTATCGCCTCGTTCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCAC 368

Qy      384 CGTCTCCTCA 393
            ||||||||||
Db      369 CGTCTCCTCA 378


RESULT 5
US-10-091-300-23
; Sequence 23, Application US/10091300
; Publication No. US20030108545A1
; GENERAL INFORMATION:
;     APPLICANT: Rockwell, Patricia
;     APPLICANT: Goldstein, Neil I.
;     TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth with a Vascular
;     TITLE OF INVENTION: Endothelial Growth Factor Receptor Antagonist
;     FILE REFERENCE: 11245/46211
;     CURRENT APPLICATION NUMBER: US/10/091,300
;     CURRENT FILING DATE: 2002-03-04
;     NUMBER OF SEQ ID NOS: 85
;     SOFTWARE: WordPerfect 8.0 for Windows
;     SEQ ID NO 23
;     LENGTH: 348
;     TYPE: DNA
;     ORGANISM: Human
US-10-091-300-23

Query Match             68.6%;    Score 269.6;  DB 14;  Length 348;
Best Local Similarity   96.8%;    Pred. No. 9.2e-80;
Matches  275;  Conservative  0;  Mismatches  9;  Indels  0;  Gaps  0;

Qy       24 GGTGGAGTCTGGGGGAGGCCCTGGTCAAGCCTGGGGACTCTCCTGTGCAGC 83
            |||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       12 GGTGCAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 71

Qy       84 CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG 143
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       72 CTCTGGATTCACCTTCAGTAGCTATAGCATGAACTGGGTCCGCCAGGCTCCAGGGAAGGG 131

Qy      144 GCTGGAGTGGGTCTCATCCATTCAATTAGTAATAGTAATAGTAATACTTACATATATACTACGCAGACACGCACCGCAGT 203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      132 GCTGGAGTGGGTCTCATCCATTAGTAGTAGTTACATATATACGGCAGACTCAGT 191

Qy      204 GAAGGGCCGATTCACCAATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      192 GAAGGGCCGATTCACCAATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 251

Qy      264 CAGCCTGAGAGCCGAGGACACACGGCTGTGTTACTACTGTGCGAGAG 307
            |||||||||||||||||||||||||||||||||||||||||||||||
Db      252 CAGCCTGAGAGCCGAGGACACACGGCTGTGTATTACGTGTGCGAGAG 295


RESULT 6
US-10-091-300-27
; Sequence 27, Application US/10091300
; Publication No. US20030108545A1
; GENERAL INFORMATION:
;     APPLICANT: Rockwell, Patricia
```

; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth With a Vascular
; TITLE OF INVENTION: Endothelial Growth Factor Receptor Antagonist
; FILE REFERENCE: 11245/46211
; CURRENT APPLICATION NUMBER: US/10/091,300
; CURRENT FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 27
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Human
US-10-091-300-27

Query Match   68.6%;   Score 269.6; DB 14; Length 348;
Best Local Similarity 96.8%; Pred. No. 9.2e-80;
Matches 275; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```
Qy    24 GGTGGAGTCTGGGGGGAGGGCCTGGTCAAGCCTGGCGGGGGGGGGGTCCCTGAGACTCTCCTGTGCCAGC 83
         |||| ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db    12 GGTGCAGTCTGGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCCAGC 71

Qy    84 CTCTGGATTCACCTTCAGTAGCTATAGCACTGGGGTCCGCCCAGGGGTCCAGGGAAGGG 143
         ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db    72 CTCTGGATTCACCTTCAGTAGCTATAGCATGCCGGGGTCCGCCCAGGGGTCCAGGGAAGGG 131

Qy   144 GCTGGAGTGGGTCTCATCCATCATTAGTAATAGTAATAACTTACATATACTACGCACGCAGT 203
         ||||||||||||||||||||||  ||||| ||||||||||||||||||||||||||||||
Db   132 GCTGGAGTGGGTCTCATCCATTAGTAGTAGTAGTTACATATACTACGCACGCAGT 191

Qy   204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTGTATCTGCAAATGAA 263
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   192 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 251

Qy   264 CAGCCTGAGAGCCGACCACGGCTGTGTACTACTGTGCGAGAG 307
         |||||||||||||||   |||| ||||||||||||||||||
Db   252 CAGCCTGAGAGCCGAGGACACGGGCTGTGTATTACTGTGCGAGAG 295
```

RESULT 7
US-10-091-300-30

; Sequence 30, Application US2003010854A1
; Publication No. US2003010854A1
; GENERAL INFORMATION:
; APPLICANT: Rockwell, Patricia
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth With a Vascular
; TITLE OF INVENTION: Endothelial Growth Factor Receptor Antagonist
; FILE REFERENCE: 11245/46211
; CURRENT APPLICATION NUMBER: US/10/091,300
; CURRENT FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 30
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Human
US-10-091-300-30

Query Match   68.2%;   Score 268; DB 14; Length 348;
Best Local Similarity 96.5%; Pred. No. 3.2e-79;
Matches 274; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

```
Qy    24 GGTGGAGTCTGGGGGGAGGCCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
         |||| ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db    12 GGTGCAGTCTGGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 71

Qy    84 CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGGTCCGCCCAGGGGTCCAGGGAAGGG 143
         ||||||||||||||||||||||||||||||  |||||||||||||||||||||||||||||
Db    72 CTCTGGATTCACCTTCAGTAGCTATAGCATGGGGTCCGCCCAGGGGTCCAGGGAAGGG 131

Qy   144 GCTGGAGTGGGTCTCATCCATTAGTAAATAGTAATAATACTTACATATATACGCACGACGCACT 203
         |||||||||||||||||||||||  |||||| |||||||||||||||||||||||||||||
Db   132 GCTGGAGTGGGTCTCATCCATTAGTAGTAGCATGAACTGGGGTCGGTCCAGGGAAGGG 191

Qy   204 CTCTGGATTCAGCTAGCTATAGCATGAACTGGGGTCGGTCCAGGGAAGGG 143
```

Db   132 GCTGGAGTGGGTCTCATCCATTCCATTAGTTAGTAGTTACATATACTACGCACGCAGT 191
Qy   204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
Db   192 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 251
Qy   264 CAGCCTGAGAGCCGAGGACACGGGCTGTGTATTACTGTGCGAGAG 307
Db   252 CAGCCTGAGAGCCGAGGACACGGGCTGTGTATTACTGTGCGAGAG 295

RESULT 8
US-10-325-694-143

; Sequence 143, Application US/10325694
; Publication No. US20030148463A1
; GENERAL INFORMATION:
; APPLICANT: KUFER, PETER
; APPLICANT: RAUM, TOBIAS
; TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
; TITLE OF INVENTION: RECEPTORS AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/325,694
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US/09/403,107
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 143
; LENGTH: 414
; TYPE: DNA
; ORGANISM: HUMAN
US-10-325-694-143

Query Match   66.9%;   Score 262.8; DB 12; Length 414;
Best Local Similarity 81.9%; Pred. No. 1.8e-77;
Matches 303; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

```
Qy    24 GGTGGAGTCTGGGGGGAGGGCCGGGCTGGGTTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCCAGC 83
         |||||||||||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||
Db    12 GCTCGAGTCTGGGGGGAGGCCTGGTCCAGCCTCCAGGGGTCCCTGAGACTCTCCTGTGCAGC 71

Qy    84 CTCTGGATTCACCTTCAGTTAGCTATAGCATGACTGGGTCCGCGCAGGCTCCAGGGAAGGG 143
         |||||||||||| |||||| |||| |||||||||  |||||||||||||||||||||||
Db    72 CTCTGGATTCACCTTCAGTAGCTATAGCATGGGGTCCGCCCAGGGAAGGG 131

Qy   144 GCTGGAGTGGGTCTCATCCATTAGTAATAATTAATAGTAATAGTACATATACTACGCACGCAGT 203
Db   132 GCTGGAGTGGGTCTGCAGTCAGTTATATCATATGATTAATATACTACGCTGGTACCGT 191

Qy   204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
Db   192 GAAGGGCCCCGATTCACCATCTCCAGAGACAACTCCAAAGAACACGCTGTATCTGCAAATGAA 251

Qy   264 CAGCCTGCTGAGAGACCGGAGACAACGGCTGTGTTCTGTACTACTGGTGATATACAGTAA 323
Db   252 CAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCTGAAAGATAATGGGGTGGGGCAG 311

Qy   324 TTTCCTCCGTTGGGTTCGGACGGGTAATGGAGACGGTGCGAAAGACGGGCAACGGTCAC 383
Db   312 TGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCAC 371

Qy   384 CGTCTCCTCA 393
Db   372 CGTCTCCTCA 381
```

RESULT 9
US-10-041-860-59

; Sequence 59, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Coryalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi

```
~ APPLICANT: Feng, Xiao
~ APPLICANT: Yang, Xiao-Dong
~ APPLICANT: Chen, Francine
~ APPLICANT: Gazit, Gadi
~ APPLICANT: Weber, Richard
~ APPLICANT: Bezabeh, Binyam
~ TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
~ TITLE OF INVENTION: THEREOF
~ FILE REFERENCE: ABGENIX.051A
~ CURRENT APPLICATION NUMBER: US/10/041,860
~ CURRENT FILING DATE: 2002-01-07
~ NUMBER OF SEQ ID NOS: 377
~ SOFTWARE: FastSEQ for Windows Version 4.0
~ SEQ ID NO 59
~ LENGTH: 379
~ TYPE: DNA
~ ORGANISM: homo sapiens
US-10-041-860-59

Query Match     66.5%;  Score 261.2;  DB 12;  Length 379;
Best Local Similarity   83.5%;  Pred. No. 6.1e-77;
Matches 309;  Conservative 0;  Mismatches 58;  Indels 3;  Gaps 1;

Qy  24 GGTGGAGTCTGGGGGAGGCGCTGGTGCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC  83
        ||||||||| || ||||||| || |||||||| ||||  |||||||||||| | ||||||||
Db  12 GGTGGAGTCGCGGGGAGGCGTGGTCCAGCCTGGGAAGTCCCTGAGACTCTCGTGTGCAGC  71

Qy  84 CTCTGGATTCACCTTCAGTAGTTATATGCACTGGGTCCGCCAGGCTCCAGGGAAGG  143
        ||||||||||||||||||||| ||| || ||||||||||||||||||||||||| ||||
Db  72 GTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGG  131

Qy 144 GCTGGAGTGGGTGGTCATCATCCATTAGTAATAGTTACACTTACATATACTACGCAGACTCCGT  203
        ||||||||||||||  ||  ||   |||  ||  |||  ||   |||||||||| ||||||
Db 132 GCTGGAGTGGGTGGCAGTTATATGATGGAAGTAATAAATACTATGCAGACTCCGT  191

Qy 204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAAATGAA  263
        ||||||||||||||||||||||||||||||  || ||||| |||||||||||||| ||||
Db 192 GAAGGGCCGATTCACCATCTCCAGAGACAACACGCTGTATCTGCAAATGAA  251

Qy 264 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATTCTAGATACAGTAA  323
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 252 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATTCTAGATACAGTAA  311

Qy 324 TTTCCTCCGTTGGGTTCGGACGTCTGGGGCCAAGGGACCACGGTCAT  383
        |||     ||||||| |||||||||||||||||||||||||||||
Db 312 T---GCTCGGTTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCAC  368

Qy 384 CGTCTCCTCA  393
        ||||||||||
Db 369 CGTCTCCTCA  378

RESULT 10
US-10-041-860-75
; Sequence 75, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
~ APPLICANT: Corvalan, Jose R.F.
~ APPLICANT: Jia, Xiao-Chi
~ APPLICANT: Feng, Xiao
~ APPLICANT: Yang, Xiao-Dong
~ APPLICANT: Chen, Francine
~ APPLICANT: Gazit, Gadi
~ APPLICANT: Weber, Richard
~ APPLICANT: Bezabeh, Binyam
~ TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
~ TITLE OF INVENTION: THEREOF
~ FILE REFERENCE: ABGENIX.051A
~ CURRENT APPLICATION NUMBER: US/10/041,860
~ CURRENT FILING DATE: 2002-01-07
~ NUMBER OF SEQ ID NOS: 377
~ SOFTWARE: FastSEQ for Windows Version 4.0
~ SEQ ID NO 75
```

```
~ LENGTH: 382
~ TYPE: DNA
~ ORGANISM: homo sapiens
US-10-041-860-75

Query Match     66.5%;  Score 261.2;  DB 12;  Length 382;
Best Local Similarity   81.6%;  Pred. No. 6.1e-77;
Matches 302;  Conservative 0;  Mismatches 68;  Indels 0;  Gaps 0;

Qy  24 GGTGGAGTCTGGGGGAGGCGCTGGTGCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC  83
        ||||||||| || |||||||| || ||||||||  || |||||||||||| | ||||||||
Db  12 GGTGGAGTCGCGGGGGAGGCGTGGTCCAGCCTGGGGGTCCCAGCCTGGGAAGTCCCAGC  71

Qy  84 CTCTGGATTCACCTTCAGTAGTTATATGCACTGGGTCCGCCAGGCTCCAGGGAAGG  143
        ||||||||||||||||||||| ||| || ||||||||||||||||||| ||| ||||
Db  72 GTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGG  131

Qy 144 GCTGGAGTGGGTCTCATCCATTAGTAATAGTTACACTTACATATACTACGCAGACTCCGT  203
        ||||||||||| |   |   | || |||  | | |  ||  ||||||| || ||||||
Db 132 GCTGGAGTGGGTGGCAATTTATATGGTGATGGAAGTAATAAATACTATGCAGACTCCGT  191

Qy 204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAAATGAA  263
        ||||||||||||||||||||||||||||||  || ||||| ||||| ||||||| |||
Db 192 GAAGGGCCGCTTCACCGTCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA  251

Qy 264 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATTCTAGATACAGTAA  323
        ||||||||||||||||||||||||||||||||||||||| ||| || |||||||||||
Db 252 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATTCTAGATACAGTAA  311

Qy 324 TTTCCTCCGTTGGGTTCGGACGTCTGGGGCCAAGGGACCACGGTCAT  383
        |||     ||||||| |||||||||||||||||||||||||||||
Db 312 TAGTGATTATCTTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCAC  371

Qy 384 CGTCTCCTCA  393
        ||||||||||
Db 372 CGTCTCCTCA  381

RESULT 11
US-10-153-382-16
; Sequence 16, Application US/10153382
; Publication No. US2003008693A1
; GENERAL INFORMATION:
~ APPLICANT: PFIZER PRODUCTS INC.
~ TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
~ FILE REFERENCE: PC23019A
~ CURRENT APPLICATION NUMBER: US/10/153,382
~ CURRENT FILING DATE: 2002-05-22
~ PRIOR APPLICATION NUMBER: 60/293042
~ PRIOR FILING DATE: 2001-05-23
~ NUMBER OF SEQ ID NOS: 39
~ SOFTWARE: PatentIn Ver. 2.1
~ SEQ ID NO 16
~ LENGTH: 1413
~ TYPE: DNA
~ ORGANISM: Homo sapiens
US-10-153-382-16

Query Match     66.0%;  Score 259.2;  DB 14;  Length 1413;
Best Local Similarity   81.0%;  Pred. No. 4.6e-76;
Matches 316;  Conservative 0;  Mismatches 68;  Indels 6;  Gaps 1;

Qy   4 GTGGAGACTCTCCTGTCAGTCTGGGGTGGGGGTGGAGTCTGGGGAGGCGTCAAGCCTGGGGGGGTCC  63
        |||   || |  |    ||    |||||||||||||||||||||||||  ||||||||||||||||
Db   4 CTGAGACTCTCCTGTCAGCCTGGGGTCTGGGGAGGTGGGAGTCTGGGGCTGAAAGCCTGGGAGGGTCC  63

Qy  64 CTGAGACTGTCAGGTCAGGTTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGGG  123
        |||||   |  ||      |||||||||||||||||||||||||||||||||||||||||||||||||
Db 109 CTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGTC  168

Qy 124 CGCCAGGGTCCAGGGGGAAGGGGCTGGAGTGGGTCTCATCCATTAGTAATAGTTAC  183
        |||||||    |||| || ||||||||||||||| |  ||    || || |  | |
Db 169 CGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATGTAGTGGTAATACTTAAT  228
```

RESULT 12
US-10-041-860-67
; Sequence 67, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 379
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-041-860-67

Query Match   65.6%; Score 258; DB 12; Length 379;
Best Local Similarity   83.0%; Pred No. 7.1e-76;
Matches 307; Conservative 0; Mismatches 60; Indels 3; Gaps 1;

[sequence alignment block]

RESULT 13
US-09-844-684-10
; Sequence 10, Application US/09844684
; Patent No. US20020142358A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: LA JOLLA INSTITUTE FOR ALLERGY AND IMMUNOLOGY
; TITLE OF INVENTION: HUMAN ANTI-CD40 ANTIBODIES AND METHODS OF MAKING SAME
; FILE REFERENCE: 21286/0276339
; CURRENT APPLICATION NUMBER: US/09/844,684
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/200,601
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 520
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-844-684-10

Query Match   63.7%; Score 250.4; DB 10; Length 520;
Best Local Similarity   81.9%; Pred No. 2.7e-73;
Matches 303; Conservative 0; Mismatches 61; Indels 6; Gaps 1;

[sequence alignment block]

RESULT 14
US-10-040-244-10
; Sequence 10, Application US/10040244
; Publication No. US20030059427A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; APPLICANT: FORCE, WALKER F.
; APPLICANT: TAKAHASHI, NOBUAKI
; APPLICANT: MIKAYAMA, TOSHIFUMI
; TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTI
; FILE REFERENCE: 021286/0272501
; CURRENT APPLICATION NUMBER: US/10/040,244
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/200,601
; PRIOR FILING DATE: 2000-4-28

PRIOR APPLICATION NUMBER: PCT/US01/13672
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: 09/844,684
PRIOR FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 3.0

SEQ ID NO 10
LENGTH: 520
TYPE: DNA
ORGANISM: Homo sapiens
US-10-040-244-10

Query Match   63.7%;   Score 250.4;   DB 14;   Length 520;
Best Local Similarity   81.9%;
Matches 303;   Conservative   0;   Mismatches 61;   Indels   6;   Gaps   1;

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Qy    24  GGTGGAGTCTCGGGGGAGGCCTGGTCTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC  83
          ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db    24  GGTGGAGTCTCGGGGGAGGCCTGGTCTCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC  83

Qy    84  CTCTGGATTCACCTTCAGTAGCTATAGCACATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG  143
          ||||||||| |||| ||| |||||||| |  |||  ||||||||||||||||||| ||||||||
Db    84  CTCTGGATTCACCTTCAGTAGCTATAGCACATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG  143

Qy   144  GCTGGAGTGGGTCTCATCCATTAGTAATAGTTACATATACTACGCAGACGAGT  203
          ||||||||||||||||||||| ||| ||||||||||||||||||| || |||||
Db   144  GCTGGAGTGGGTCTCATCCATTAGTAATAGTTACATATACTACGCAGACGAGT  203

Qy   204  GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA  263
          |||||||||||||||||||||||||||||||||||||||||||| |||||||| ||||||||
Db   204  GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA  263

Qy   264  CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATTCTAGATACAGTAA  323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||      ||||
Db   264  CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGAT      ATTAC  305

Qy   324  TTTCCTCCGTTGGGTTCGGGGACGGGTATGGACGGTCTGGGGCCAAGGGACCACGGTCAT  383
          |  || |||  |||| ||||||||| |||||| |||||||||||||||||||||||||||||
Db   306  TATGGTTCGGGGAGTTATGAAGGAGTTATGGGGGGCCAAGGGACCACGGTCAC  365

Qy   384  CGTCTCCTCA  393
          ||||||||||
Db   366  CGTCTCCTCA  375
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RESULT 15
US-10-172-317-1
Sequence 1, Application US/10172317
Publication No. US20030091561A1
GENERAL INFORMATION:
APPLICANT: van de Winkel, Jan G.J.
APPLICANT: van Dijk, Marcus A.
APPLICANT: Halk, Edward
APPLICANT: Gerritsen, Arnout F.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO
TITLE OF INVENTION: EPIDERMAL GROWTH FACTOR RECEPTOR (EGFR)
FILE REFERENCE: GMI-020
CURRENT APPLICATION NUMBER: US/10/172,317
CURRENT FILING DATE: 2002-06-13
PRIOR APPLICATION NUMBER: US 60/298,172
PRIOR FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1
LENGTH: 375
TYPE: DNA
ORGANISM: Homo sapiens
US-10-172-317-1

Query Match   63.3%;   Score 248.8;   DB 14;   Length 375;
Best Local Similarity   81.6%;
Matches 302;   Conservative   0;   Mismatches 62;   Indels   8;   Gaps   0;

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Qy    24  GGTGGAGTCTCGGGGGAGGCCTGGTCTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC  83
          ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db    12  GGTGGAGTCTCGGGGGAGGCCTGGTCTCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC  71

Qy    84  CTCTGGATTCACCTTCAGTAGCTATAGCACATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG  143
          ||||||||| |||| ||| |||||||| |  |||  ||||||||||||||||||| ||||||||
Db    72  GTCTGGATTCACCTTCAGTAGCTATAGCACATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG  131

Qy   144  GCTGGAGTGGGTCTCATCCATTAGTAATAGTTACATATACTACGCAGACGAGT  203
          ||||||||||||||||| ||||||||||||| |||||||||||| ||| |||||
Db   132  GCTGGAGTGGGTCTCATCCATTAGTAATAGTTACATATACTACGCAGACGAGT  191

Qy   204  GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA  263
          ||||||||||||||||||||||||||||||||||||||||||||| ||||||| ||||||||
Db   192  GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA  251

Qy   264  CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATTCTAGATACAGTAA  323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||      ||||
Db   252  CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGAT      ATTAC  305

Qy   324  TTTCCTCCGTTGGGTTCGGGGACGGGTATGGACGGTCTGGGGCCAAGGGACCACGGTCAT  383
          |  || |||  |||| |||||||| ||||||| ||||||||||||||||||||||||||||
Db   306  TATGGTTCGGGGAGTTATGAAGGAGTTATGGGGGGCCAAGGGACCACGGTCAC  365

Qy   384  CGTCTCCTCA  393
          ||||||||||
Db   366  CGTCTCCTCA  375
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RESULT 16
US-09-918-995-16657
Sequence 16657, Application US/09918995
Publication No. US20030076623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 16657
LENGTH: 407
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(407)
OTHER INFORMATION: n = A,T,C or G
US-09-918-995-16657

Query Match   63.1%;   Score 248;   DB 11;   Length 407;
Best Local Similarity   94.5%;
Matches 257;   Conservative   0;   Mismatches 15;   Indels   0;   Gaps   0;

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Qy    24  GGTGGAGTCTCGGGGGAGGCCTGGTCTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC  83
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   135  GGTGGAGTCTCGGGGGAGGCCTGGTCTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC  194

Qy    84  CTCTGGATTCACCTTCAGTAGCTATAGCACATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG  143
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   195  CTCTGGATTCACCTTCAGTAGCTATAGCACATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG  254

Qy   144  GCTGGAGTGGGTCTCATCCATTAGTAATAGTTACATATACTACGCAGACGAGT  203
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   255  GCTGGAGTGGGTCTCATCCATTAGTAATAGTTACATATACTACGCAGACGAGT  314

Qy   204  GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA  263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   315  GAAGGGCCGCTTCACCATCTCCAGAGACAACTCACTGTATCTGCAAATGAA  374
```

```
Qy     264  CAGCCTGAGAGCCGAGACCACACGGCGCTGTGTACT 295
            ||||||||||||||||||||||||||| |||||||| |
Db     375  CAGCCTGAGAGCCGAGGACACGGCTCTGTGTATT 406
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Qy     384  CGTCTC 389
            |||||||
Db     366  CGTCTC 371
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RESULT 17
US-10-039-785-65
; Sequence 65, Application US/10039785
; Publication No. US20020067646A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 747
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding T1006F07 scFv
US-10-039-785-65

Query Match   63.1%; Score 248; DB 13; Length 747;
Best Local Similarity 82.0%; Pred. No. 2e-72;
Matches 300; Conservative 0; Mismatches 60; Indels 6; Gaps 1;

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Qy      24  GGTGGAGTCTGGGGAGGCCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
            ||||||||| | |||  ||||||||||||||||||||||||||||||||||| |||||||
Db      12  GTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 71

Qy      84  CTCTGGATTCACCTTCAGTAGCTATAAGCACATGCACTGGGTCCGCCAGGCTCCAGGAAGG 143
            ||||||||||||| ||| | ||||||| ||||  ||||||||||| |||||||||| ||||
Db      72  CTCTGGATTCACCTTTAGCAACTATGCCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGG 131

Qy     144  GCTGGAGTGGGTCTCATCCATTAGTAATAGTAATAATACTTACATATACTACGCAGACGAGCACT 203
            | |||||||||||| |  |||| | ||| |||||||   |||| | |||||||| | |||| |
Db     132  GCTGGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCAGACTCCGT 191

Qy     204  GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
            |||||| | |||||||| || | |  |||||||| ||||||||||| | |||||||||||
Db     192  GAAGGGCCGGTTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 251

Qy     264  CAGCCTGAGAGCCGAGGACACGGCTGTGTACTACTGTGCGAGAGATTCTAGATACAGTGA 323
            ||||||||||||| || || ||||| |||||||||| ||| ||||| | | | ||| ||
Db     252  CAGCCTGAGAGACCGAGGACACGGCCGTGTATTACTGTGCGAGAGAACCATCCTTTCAGCA 311

Qy     324  TTTCTCCCGTTGCGGACGACGGTGATGGACGTCTGGGGCCAAGGGACCACGGTCAT 383
            |||| || || ||   |  || |||||||| |||  | ||||||||| || |
Db     312  GTGGGGCCACT-----ACTCCTAGGGTATGGACGGACGTCTGGGGCCAGGGGACAATGGTCAC 365
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RESULT 18
US-09-964-824A-583
; Sequence 583, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Horrigan, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-73
; CURRENT APPLICATION NUMBER: US/09/964,824A
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/60/236,033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,028
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 583
; LENGTH: 527
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-824A-583

Query Match   63.0%; Score 247.6; DB 10; Length 527;
Best Local Similarity 77.2%; Pred. No. 2.4e-72;
Matches 301; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

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Qy       4  GTGCAGCTGCTCGAGTCTGGGGGTGGAGTCTGGGGAGGCCCTGGTCAAGCCTGGGGGGTCC 63
            ||||||| ||  ||||| |||||  |||||||||||||||||||||||||||||||||||
Db      43  GTCCAGTGTCAGGTCAGCCTGGTGGGGAGTCTGGGGAGGCGTGGTCCCAGCCTGGGGAGGTCC 102

Qy      64  CTGAGACTCTCCTGTGCAGCCCTCTGGATTCACCTTCAGTAGCTATTAGCATGCACTGGGTC 123
            ||||||||||||  |||  | | | ||||||  ||  || ||  |||  || || ||||||
Db     103  CTGAGACTCTCCTGTGCAGTCTCTGGACTCACCTTTAGTAGCTATGGCTATGCACTGGGTC 162

Qy     124  CGCCAGGGTCCAGGGAAGGGGCTGGAGTGGGTCTCATCCATTAGTAATAGTAATAGTTAC 183
            |||||| | ||| ||  ||   ||||||||| || | |||  ||||| |  ||| | |
Db     163  CGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATTAGTAGTAGGAAGTAAT 222

Qy     184  ATATACTACGCAGACAGTGAAGGGCCGATTCACCATCTCCAGAGACAACACGCCAAGAAC 243
            ||  ||||| | | |||||||| ||||||||| || || | | ||||| |||||| |||
Db     223  AAATACTACGGCAGACTCCTTGAAGGGCCGATTCACCATCTCCAGAGACAACATTCCAAGAAC 282

Qy     244  TCACTGTATCTGCAAATGAACAGCCTGAGAGCCGAGCACACGACACGGCTGTGTACTACTGTGCG 303
            |||| | || | |||||||||| ||||||||| | | | |||| | ||| |||| ||||  |
Db     283  ACGCTGTATCTGCAAATGAACAGCCTGAGATCTGAGGACACGGCTGTGTATTACTGTGCG 342

Qy     304  AGAGATTCTAGATACAGTGATTTCCTCCCGTTGGGTTCGGGACGACGGTTATGGACGTCTGG 363
            |||| | |  | | |  | | ||  | |  || |||  | ||| || |||||  ||||||
Db     343  AGAGGGGGGGGGGATTACTGATTTTGGAGTGGTTATTACGGTCAAGTGGTTCGACCCCTGG 402

Qy     364  GGCCAAGGGGACCACGGTCATCCTCTCCTCA 393
            ||||| |||||| ||||| | | |  |||||
Db     403  GGCCAGGGGGAACCCTGGTCACCGTCTCCTCA 432
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RESULT 19
US-09-954-456-1188
; Sequence 1188, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456

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;  CURRENT FILING DATE: 2001-09-18
;  PRIOR APPLICATION NUMBER: US/60/233,617
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US/60/234,052
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,923
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,134
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,637
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,638
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,711
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,720
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,840
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,863
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 2276
;  SOFTWARE: Patentin version 3.0
;
;  SEQ ID NO 1188
;      LENGTH: 527
;      TYPE: DNA
;      ORGANISM: Homo sapiens
US-09-954-456-1188

Query Match     63.08%;   Score 247.6;  DB 10;   Length 527;
Best Local Similarity    77.2%;   Pred. No. 2.4e-72;
Matches 301;  Conservative   0;  Mismatches 89;  Indels  0;  Gaps  0;

Qy         4 GTGCAGCTGCTCGAGTCTGGGGGTGGAGTCTGGGGGGAGGCCTGGTCAAGCCTGGGGGGTCC  63
             ||  ||  | |  ||||| |||  ||| || ||||||||| ||||||||||||||| |||||
Db        43 GTCCAGCGTGCAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCC  102

Qy        64 CTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTC  123
             ||| || ||| || || |||||||||| |||||||| || ||| |||||||| ||||||||
Db       103 CTGAGACTCTCCTGTGCAGTCTCTGGATTCACCTTTAGTAGCTATGATATGCACTGGGTC  162

Qy       124 CGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTGGGTCTCATCCATTAGTAATAGTAATTTAC  183
             || || |||||||| || |||||| ||||| || ||   || |||  |||| |||||  |||
Db       163 CGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGGTTATCATATGATGGAAGTAAT  222

Qy       184 ATATACTACGCAGACAGCAGTGAAGGGCCGGATTCACCATCTCCAGAGACAACGCCAAGAAC  243
             | ||||| |||||||  ||| ||  ||||||||| ||||||||| ||||| ||| ||||||
Db       223 AAATACTACGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAAC  282

Qy       244 TCACTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTACTACTGTGCG  303
             |||||| ||| || |||||||| ||| ||||| ||||| ||| || | |||||||||||
Db       283 ACGCTGTATCTGCAAATGAACAGCCTGAGAGATGAGGACACGGCTGTGTATTACTGTGCG  342

Qy       304 AGAGATTCTAGATACACAGTAAATTTCCTCCGTTGGGTTCGGAGCGACGGTATGGACGTCTGG  363
             ||||  |  |   ||||||     |||| ||||  ||  |||||  ||||||||||
Db       343 AGAGGGCGGGGAGATTACGTGATTTTTTGGAGTGGTTATTACGTCAACTGGTTCGACCCCTGG  402

Qy       364 GGCCAAGGGACCACGGTCATCGTCTCCTCA  393
             ||||| ||||| ||| ||||||||||||||
Db       403 GGCCAGGGGAACCCTGGTCACCGTCTCCTCA  432
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;  CURRENT FILING DATE: 2001-10-05
;  NUMBER OF SEQ ID NOS: 135
;  SOFTWARE: Patentin version 3.0
;
;  SEQ ID NO 73
;      LENGTH: 666
;      TYPE: DNA
;      ORGANISM: Homo sapiens
;      FEATURE:
;      NAME/KEY: CDS
;      LOCATION: (1)..(666)
US-09-972-656-73

Query Match     62.7%;   Score 246.4;  DB 11;   Length 666;
Best Local Similarity    92.5%;   Pred. No. 6.5e-72;
Matches 259;  Conservative   0;  Mismatches 21;  Indels  0;  Gaps  0;

Qy        24 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC  83
             |||||| ||||||||||||| ||||||||||||||||||| ||||||||||||||||||||
Db        12 GCTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC  71

Qy        84 CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG  143
             |||||||||||||||||| || ||| ||||||| ||||||||||||||||||||| ||||
Db        72 CTCTGGATTCACCTTCAGTAGCTATAGCATGAACTGGGTCCGCCAGGCTCCAGGGAAGGG  131

Qy       144 GCTGGAGTGGGTCTCATCCATTAGTAATAGTAATAATACTTACATATACTACGCAGACAGT  203
             ||||||||||| |||||||||||||||||||||| ||   |||||||||||||||||| ||
Db       132 GCTGGAGTGGGTCTCATCCATTAGTAGTAATGGGTAGCAGTTACAGATTACGACGCGCAGT  191

Qy       204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA  263
             ||| ||||||||||||||||||||||||||   ||||||||| ||||| ||||||||||
Db       192 GAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAA  251

Qy       264 CAGCCTGAGAGCCGAGGACACGGCTGTGTACTACTGTGCG  303
             ||||||||||| |||||||||||| | || |||||||||
Db       252 TAGCCTGAGAGCCGAGGACACGGCCGTATTACTGTGCG  291
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Search completed: September 24, 2003, 06:25:28
Job time : 1827 secs

RESULT 20
US-09-972-656-73
Sequence 73, Application US/09972656
Publication No. US20030099647A1
GENERAL INFORMATION:
APPLICANT:
APPLICANT: Deshpande, Rajendra
APPLICANT: Tsai, Mei-Mei
TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
TITLE OF INVENTION: Neutralizing Activity
FILE REFERENCE: A-799
CURRENT APPLICATION NUMBER: US/09/972,656

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OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: September 24, 2003, 03:23:09 ; Search time 3359 seconds
                 (without alignments)
                 3880.133 Million cell updates/sec

Title: US-09-848-798A-97
Perfect score: 393
Sequence: 1 gaggtgcagctgctcgagtc.........ccacggtcatcgtctcctca 393

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 3336 3688 seqs, 1658 1889874 residues

Total number of hits satisfying chosen parameters: 66727376

Post-processing: Minimum Match 0%
Maximum DB seq length: 0   Maximum Match 100%
Minimum DB seq length: 2000000000   Listing first 60 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	393	100.0	US-09-848-798-97	Sequence 97, Appl
2	393	100.0	US-09-848-798A-97	Sequence 97, Appl
3	363.6	92.5	US-09-848-798-96	Sequence 96, Appl
4	363.6	92.5	US-09-848-798A-96	Sequence 96, Appl

5	272.2	69.3	311	48	36	US-09-864-761-31233	Sequence 31233, A
6	272.2	69.3	311	48		US-5-10-203-135-20914	Sequence 20914, A
7	272.2	69.3	311	48		US-5-10-203-135-21308	Sequence 21308, A
8	272.2	69.3	2091	47		US-10-170-235-30772	Sequence 30772, A
9	272.2	69.3	96			US-60-415-024-32	Sequence 32, Appl
10	271.8	69.2	375	68		US-60-141-701-3	Sequence 3, Appl
11	271.2	69.0	819	1		PCT-US02-18947-198	Sequence 198, App
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14	271.2	69.0	819	45		US-10-062-188-6	Sequence 6, Appli
15	271.2	69.0	819	47		US-10-172-118-198	Sequence 198, App
16	271.2	69.0	819	50		US-10-342-887-198	Sequence 198, App
17	271.2	69.0	819	102		US-60-474-850-84	Sequence 84, Appl
18	270.8	68.9	379	1		PCT-US03-00398-55	Sequence 55, Appl
19	270.8	68.9	379	2		PCT-US03-00398-55	Sequence 55, Appl
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21	270.2	68.8	294	49		US-10-251-215-17	Sequence 17, Appl
22	269.6	68.6	348	1		PCT-US02-06762-23	Sequence 23, Appl
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48	262.2	66.6	414	50		US-10-325-694-143	Sequence 143, App
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Query Match   100.0%;   Score 393;   DB 35;   Length 393;
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Matches   393;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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; RESULT 3
US-09-848-798-96

; Sequence 96, Application US/0848798
; GENERAL INFORMATION:
;   APPLICANT: Siegel, Donald L.
;   TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;   TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;   FILE REFERENCE: 09596-4202
;   CURRENT APPLICATION NUMBER: US/09,848,798
;   CURRENT FILING DATE: 2001-05-04
;   PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
;   PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
;   PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
;   PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
;   NUMBER OF SEQ ID NOS: 224
;   SOFTWARE: Patentin Ver. 2.0
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; SEQ ID NO 96
;   LENGTH: 381
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain E01
US-09-848-798-96

Query Match   92.5%; Score 363.6; DB 35; Length 381;
Best Local Similarity   98.9%; Pred. No. 2e-96;
Matches 366; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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US-09-848-798A-96

; Sequence 96, Application US/0848798A
; GENERAL INFORMATION:
;   APPLICANT: Siegel, Donald L.
;   TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;   TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;   FILE REFERENCE: 09596-4202
;   CURRENT APPLICATION NUMBER: US/09,848,798A
;   CURRENT FILING DATE: 2001-05-04
;   PRIOR APPLICATION NUMBER: 09/240,274
;   PRIOR FILING DATE: 1999-05-02
;   PRIOR APPLICATION NUMBER: 60/028,550
;   PRIOR FILING DATE: 1996-10-11
;   NUMBER OF SEQ ID NOS: 224
;   SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 96
;   LENGTH: 381
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain E01
US-09-848-798A-96

Query Match   92.5%; Score 363.6; DB 35; Length 381;
Best Local Similarity   98.9%; Pred. No. 2e-96;
Matches 366; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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; RESULT 5
US-09-864-761-31233

; Sequence 31233, Application US/0864761

Left column

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;  GENERAL INFORMATION:
;  APPLICANT:  Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION:  HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Acomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE:  2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE:  2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE:  2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE:  2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE:  2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
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;  PRIOR APPLICATION NUMBER: PCT/US01/00667
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;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE:  2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE:  2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE:  2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE:  2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE:  2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE:  2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE:  2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE:  2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
;  SEQ ID NO 31233
;  LENGTH: 311
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  OTHER INFORMATION:  MAP TO AB019439.1
;  FEATURE:
;  OTHER INFORMATION:  EXPRESSED IN LUNG, SIGNAL = 0.42
;  FEATURE:
;  OTHER INFORMATION:  EXPRESSED IN ADULT LIVER, SIGNAL = 0.51
;  FEATURE:
;  OTHER INFORMATION:  EST_HUMAN HIT: AW403220.1, EVALUE 0.00e+00
;  OTHER INFORMATION:  NT HIT: L29155.1, EVALUE 0.00e+00
;  OTHER INFORMATION:  SWISSPROT HIT: P01764, EVALUE 3.00e-43
US-09-864-761-31233
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Query Match        69.3%;      Score 272.2;   DB 36;   Length 311;
Best Local Similarity 97.2%;   Pred. No. 1.9e-69;
Matches   277;  Conservative   0;  Mismatches   8;  Indels   0;  Gaps   0;

Qy    24 GGTGGGACTCTGGGGGAGGGCCCTGGGTCCAAGCCTCTGGGGGGGGTTCCCCCAGGGTCCCTGAGACTCTCCCTGTTGCAGC  83
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    23 GGTGGGAGTCTGGGGGAGGGCCCTGGTCAAGCCTCTGGGGGGGGTTCCCCCTGAGACTCTCCCTGTTGCAGC  82

Qy    84 CTCTGGGATTCACCTTCAGTAGGCTATAACCATCCACTGGGTCCCCCAGGGTCCAGGGAAGGG  143
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    83 CTCTGGGATTCACCTTCAGTAGCTATAAGCATGAACTGGGTCCGCCCAGGGCTCCAGGGAAGG  142
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Right column

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Qy   144 GCTGGGAGTGGGTGTCTCATCCCATTTAGTAATAGTAAATACTTTACATATAACTAGGCCAGAGACGCAGT  203
         ||||||||||||||||||||| ||||||||||||||||||||||| ||||||||||||||||||||| |||
Db   143 GCTGGGAGTGGGTGTCTCATCCATCCCATTTAGTAGTAGTAGTAGTTACATATAACTAGGCCAGAGACTCAGT  202

Qy   204 GAAGGGCCGGATTCACCATCTCCAGAGAGACAAAGCCGCCAAGAAACTCACTGTATCTGTCAAAATGAA  263
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   203 GAAGGGCCGGATTCACCATCTCCAGAGACACACGCCAAGAAACTCACTGTATCTGCAAAATGAA  262

Qy   264 CAGCCTGAGACCCGAGCCACACGGGCCTGTTACTACGTGTGCCGAGAGA  308
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   263 CAGCCTGAGACGCGAGCACGACACGCCGTGTGTTAACTACGTGTGCGAGAGA  307
```

```
RESULT 6
US-10-203-135-20914
;  Sequence 20914, Application US/10203135
;  GENERAL INFORMATION:
;  APPLICANT:  Molecular Dynamics, Inc.
;  APPLICANT:  Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION:  HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
;  TITLE OF INVENTION:  ANALYSIS OF GENE EXPRESSION IN HUMAN LUNG
;  FILE REFERENCE: PB 0004 WO 5
;  CURRENT APPLICATION NUMBER: US/10/203,135
;  CURRENT FILING DATE:  2002-08-02
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE:  04 February 2000 (04.02.00)
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE:  26 May 2000 (26.05.00)
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE:  03 August 2000 (03.08.00)
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE:  03 October 2000 (03.10.00)
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE:  27 September 2000 (27.09.00)
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE:  21 September 2000 (21.09.00)
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE:  30 June 2000 (30.06.00)
;  NUMBER OF SEQ ID NOS: 37012
;  SOFTWARE: Molecular Dynamics Sequence Listing Engine
;  SEQ ID NO 20914
;  LENGTH: 311
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  OTHER INFORMATION:  MAP TO AB019439.1
;  FEATURE:
;  OTHER INFORMATION:  EXPRESSED IN LUNG, SIGNAL = 0.42
;  FEATURE:
;  OTHER INFORMATION:  EST_HUMAN HIT: AW403220.1, EVALUE 0.00e+00
;  FEATURE:
;  OTHER INFORMATION:  NT HIT: L29155.1, EVALUE 0.00e+00
;  OTHER INFORMATION:  SWISSPROT HIT: P01764, EVALUE 3.00e-43
US-10-203-135-20914
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Query Match        69.3%;      Score 272.2;   DB 48;   Length 311;
Best Local Similarity 97.2%;   Pred. No. 1.9e-69;
Matches   277;  Conservative   0;  Mismatches   8;  Indels   0;  Gaps   0;

Qy    24 GGTGGAGTCTGGGGGAGGGCCGGCCCTGGGTCAAGCCTCTGGGGGGGGGTCCCCTGAGACTCTCCCTGTTGCAGC  83
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    23 GGTGGAGTCTGGGGGAGGGCCTGGGTCAAGCCTCTGGGGGGGGGTCCCCCTGAGACTCTCCCTGTTGCAGC  82

Qy    84 CTCTGGGATTCACCTTCAGTAGCTATAGCATGAACATGCACTGGGTCGGCCAGGGTCCAGGGAAGGG  143
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    83 CTCTGGGATTCACCTTCAGTAGCTATAAGCATGAACTGGGTCCGCCCAGGGCTCCAGGGAAGG  142

Qy   144 GCTGGGAGTGGGGTCGATCCATTCCATTAGTAATAGTAAATACTTTACATATAACTACTACGCGAGACGCGAGT  203
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   144 GCTGGGAGTGGGTGTCGATCCATCCCATTAGTAATAGTAAATACTTTACATATAACTACTACGCGAGACGCAGT  203
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RESULT 7
US-10-203-136-21308
Sequence 21308, Application US/10203136
; GENERAL INFORMATION:
;   APPLICANT: Molecular Dynamics, Inc.
;   APPLICANT: Penn, Sharron G.
;   APPLICANT: Rank, David R.
;   APPLICANT: Hanzel, David K.
;   APPLICANT: Chen, Wensheng
;   TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;   TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER
;   FILE REFERENCE: PB 0004 WO 3
;   CURRENT APPLICATION NUMBER: US/10,203,136
;   CURRENT FILING DATE: 2002-08-02
;   PRIOR APPLICATION NUMBER: US 60/180,312
;   PRIOR FILING DATE: .04 February 2000 (04.02.00)
;   PRIOR APPLICATION NUMBER: US 60/207,456
;   PRIOR FILING DATE: 03 October 2000 (03.10.00)
;   PRIOR APPLICATION NUMBER: US 60/236,359
;   PRIOR FILING DATE: 26 May 2000 (26.05.00)
;   PRIOR APPLICATION NUMBER: US 09/632,366
;   PRIOR FILING DATE: 03 August 2000 (03.08.00)
;   PRIOR APPLICATION NUMBER: GB 24263.6
;   PRIOR FILING DATE: 27 September 2000 (27.09.00)
;   PRIOR APPLICATION NUMBER: US 60/234,687
;   PRIOR FILING DATE: 21 September 2000 (21.09.00)
;   PRIOR APPLICATION NUMBER: US 09/608,408
;   PRIOR FILING DATE: 30 June 2000 (30.06.00)
;   NUMBER OF SEQ ID NOS: 38578
;   SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 21308
;   LENGTH: 311
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AB019439.1
;   FEATURE:
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.51
;   FEATURE:
;   OTHER INFORMATION: EST_HUMAN HIT: AW403220.1, EVALUE 0.00e+00
;   FEATURE:
;   OTHER INFORMATION: NT HIT: L29155.1, EVALUE 0.00e+00
;   FEATURE:
;   OTHER INFORMATION: SWISSPROT HIT: P01764, EVALUE 3.00e-43
US-10-203-136-21308

  Query Match             69.3%;  Score 272.2;  DB 48;  Length 311;
  Best Local Similarity   97.2%;  Pred. No. 1.9e-69;
  Matches  277;  Conservative   0;  Mismatches   8;  Indels   0;  Gaps   0;

Qy          24 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTTCCCTGAGACTCTCCTTGTGCAGC 83
               ||||||||||||||||||||||||||| |||||||| |||| ||||||||||| ||||||||
Db          23 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTTCCCTGAGACTCTCCTTGTGCAGC 82

Qy          84 CTCTGGATTCACCTTCAGTAGCTATAGCACTGGGTCCGCCCAGGGTTCCAGGGAAGG 143
               ||||||||||||||||||||||||| |||||||| |||||| ||||||||||||||
Db          83 CTCTGGATTCACCTTCAGTAGCTATAGCACTGGGTCCGCCCAGGGTCCAGGGAAGG 142

Qy         144 GCTGGAGTGGGGTCTCATCCATTAGTAATAGTTACATTAACTTACACGACACGCAGT 203
               |||||||| ||| |||||||||||||||||||||||||||||||| ||||| |||||
Db         143 GCTGGAGTGGGGTCTCATCCATTAGTAGTAGTTACATTAACTACCAGGACTCAGT 202

Qy         204 GAAGGGCCGATTCACCATCTCCAGAGACAAGCCAAGAACTCACTGTATCTGCAAATGAA 263
               ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db         203 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 262

Qy         264 CAGCCTGAGAGCCGAGGACACGGCCGTGTGTTACTGTGCGAGA 308
               |||||||||||||||||||||||||||||||||||||||||||
Db         263 CAGCCTGAGAGCCGAGGACACGGCCGTGTTATTACTGTGCGAGAGA 307
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```
RESULT 8
US-10-170-235-30772
Sequence 30772, Application US/10170235
; GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig
;   TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HU
;   TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
;   FILE REFERENCE: CL001380
;   CURRENT APPLICATION NUMBER: US/10/170,235
;   CURRENT FILING DATE: 2003-03-17
;   NUMBER OF SEQ ID NOS: 42514
; SEQ ID NO 30772
;   LENGTH: 2091
;   TYPE: DNA
;   ORGANISM: HUMAN
US-10-170-235-30772

  Query Match             69.3%;  Score 272.2;  DB 47;  Length 2091;
  Best Local Similarity   97.2%;  Pred. No. 3.6e-69;
  Matches  277;  Conservative   0;  Mismatches   8;  Indels   0;  Gaps   0;

Qy          24 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTTCCCTGAGACTCTCCTTGTGCAGC 83
               ||||||||||||||||||||||||||| |||||||| |||| |||||||||||||||||||
Db         128 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTTCCCTGAGACTCTCCTTGTGCAGC 187

Qy          84 CTCTGGATTCACCTTCAGTAGCTATAGCACTGGGTCCGCCCAGGGTTCCAGGGAAGG 143
               ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db         188 CTCTGGATTCACCTTCAGTAGCTATAGCACTGGGTCCGCCCAGGGTCCAGGGAAGGG 247

Qy         144 GCTGGAGTGGGGTCTCATCCATTAGTAATAGTTACATTAACTTACACGACACGCAGT 203
               |||||||| ||| |||||||||||||||||||| |||||||||||| |||||||||||
Db         248 GCTGGAGTGGGGTCTCATCCATTAGTAGTAGTTACATTAACTACCAGGACTCAGT 307

Qy         204 GAAGGGCCGATTCACCATCTCCAGAGACAAGCCAAGAACTCACTGTATCTGCAAATGAA 263
               ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db         308 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 367

Qy         264 CAGCCTGAGAGCCGAGGACACGGCCGTGTGTTACTGTGCGAGA 308
               |||||||||||||||||||||||||||||||||||||||||||
Db         368 CAGCCTGAGAGCCGAGGACACGGCCGTGTTATTACTGTGCGAGAGA 412
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```
RESULT 9
US-60-415-024-32
Sequence 32, Application US/60415024
; GENERAL INFORMATION:
;   APPLICANT: Jolly, Chris
;   TITLE OF INVENTION: Immunoglobulin Compositions and Methods
;   FILE REFERENCE: 13311.1001
;   CURRENT APPLICATION NUMBER: US/60/415,024
;   CURRENT FILING DATE: 2002-09-30
;   NUMBER OF SEQ ID NOS: 39
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
;   LENGTH: 200000
;   TYPE: DNA
;   ORGANISM: Human
US-60-415-024-32

  Query Match             69.3%;  Score 272.2;  DB 96;  Length 200000;
  Best Local Similarity   97.2%;  Pred. No. 1.5e-68;
  Matches  277;  Conservative   0;  Mismatches   8;  Indels   0;  Gaps   0;

Qy          24 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTTCCCTGAGACTCTCCTTGTGCAGC 83
```

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Db  197586  GGTGGGAGTCTGGGGGAGGGCCTGGTCCAAGCCTGGGGGGTCCCCGCCCTGAGACTCTCCTGTGCAGC
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      84  CTCTGGATTCACCTTCAGTAGCTATAGCACTTGGGTCCGCCAGGCTCCAGGGAAGGG  143
Db  197646  CTCTGGATTCACCTTCAGTAGCTATAGCACTGGGTCCGCCAGGCTCCAGGGAAGGG  197705
Qy     144  GCTGGAGTGGGTGTCTCATCCATTAGTAATAGTAATAACTTACATAACTACGCAGACGCGAGT  203
Db  197706  GCTGGAGTGGGTCTCATCCATTAGTAGTAGTTACATATACATAACTACGCAGACTCAGT  197765
Qy     204  GAAGGGCCGATTCACCATCTCCAGAGACACAGGCCAAGAACTCACTGTATCTCCAAATGAA  263
Db  197766  GAAGGGCCGATTCACCATCTCCAGAGACAACGGCCAAGAACTCACTGTATCTCCAAATGAA  197825
Qy     264  CAGCCTGAGAGCGCGAGCACACGGCCGCTGTGTTACTACTGTGTGCGAGAGA  308
Db  197826  CAGCCTGAGAGCCGGAGGACACGGCCGCTGTGTATTACTACTGTCGCGAGAGA  197870
```

RESULT 10
US-60-141-701-3
; Sequence 3, Application US/60141701
; GENERAL INFORMATION:
;   APPLICANT: Watkins, Brynmore
;   APPLICANT: Reitz, Jr, Marvin
;   TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HIV-1 ENVELOPE
;   TITLE OF INVENTION: GLYCOPROTEIN GP120
;   FILE REFERENCE: 2026-4284
;   CURRENT APPLICATION NUMBER: US/60/141,701
;   CURRENT FILING DATE: 1999-06-30
;   NUMBER OF SEQ ID NOS: 100
;   SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 375
;   TYPE: DNA
;   ORGANISM: Human Immunodeficiency virus type 1
;   FEATURE:
;   OTHER INFORMATION: VH
US-60-141-701-3

Query Match   69.2%; Score 271.8; DB 68; Length 375;
Best Local Similarity 86.1%; Pred. No. 2.7e-69;
Matches 316; Conservative 0; Mismatches 42; Indels 9; Gaps 1;

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Qy     27  GGAGTCTGGGGGAGGGCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTC   86
Db     18  GGAGTCGGGGGAGGCCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTC   77
Qy     87  TGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGGGCT  146
Db     78  TGGATTCACCTTCAGTAACTATAGCATGCATTGGGTCCGCCAGGCTCCAGGGAAGGGGCT  137
Qy    147  GGAGTGGGTCTCATCCATTAGTAAATACTTACATAATACGCACAGACGCGAGTGAA  206
Db    138  GGAGTGGGATTTCATACAATTACTTAGTAGTGCCATAATACTACCAGACTCTGTGAA  197
Qy    207  GGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAACAG  266
Db    198  GGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAACAG  257
Qy    267  CCTGAGAGCCGAGGACACGGCTGTGTACTACTGTGCGAGAGATTCTAGATACAGTAATTT  326
Db    258  CCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATTTAATGGGTGGTGGCAT  317
Qy    327  CCTCCGTTGGGTTCGGAGGCGACGGCTATGGACGTCTCGGGGCCAAGGGACCACGGTCATCGT  386
Db    318  TGGCTACT-------------CCTACGGTGTGGACCTCTGGGGCCAAGGGACCACGGTCACCGT  368
Qy    387  CTCCTCA  393
Db    369  CTCCTCA  375
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RESULT 11
PCT-US02-18947-198
; Sequence 198, Application PC/TUS0218947
; GENERAL INFORMATION:
;   APPLICANT: Rosetta Inpharmatics
;   TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
;   FILE REFERENCE: 9301-175-228
;   CURRENT APPLICATION NUMBER: PCT/US02/18947
;   CURRENT FILING DATE: 2002-06-14
;   PRIOR APPLICATION NUMBER: 60/380,770
;   PRIOR FILING DATE: 2002-05-14
;   NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 198
;   LENGTH: 819
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: AJ225092
;   DATABASE ENTRY DATE: 2001-06-18
PCT-US02-18947-198

Query Match   69.0%; Score 271.2; DB 1; Length 819;
Best Local Similarity 86.2%; Pred. No. 5.2e-69;
Matches 319; Conservative 0; Mismatches 33; Indels 18; Gaps 1;

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Qy     24  GGTGGAGTCTGGGGGAGGGCCTGGTCAAGCCTGGGGGGGGTCCCTGAGACTCTCCTGTGCAGC   83
Db     18  GGTGGAGTCTCGGGGGAGGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC   77
Qy     84  CTCTGGATTCACCTTCAGTAGCTATAGCACTGGGTCCGCCAGGGTCCAGGGAAGGG  143
Db     78  CTCTGGATTCACCTTCAGTAACTATAGCATGCATGAACTATAGCAGACGCGAGGGTCCCGCCAGGGTCCAGGGAAGGG  137
Qy    144  GCTGGAGTGGGTGTCTCATCCATTAGTAATAGTAATAACTTACATAATACGCACAGACGCGAGT  203
Db    138  GCTGGAGTGGGTCTCATCCATTAGTAGTAGTTACATAATACTACCAGACTTCCT  197
Qy    204  GAAGGGCCGATTCACCATCTCCAGAGACAACAACGCCAAGAACTCACTGTATCTGCAAATGAA  263
Db    198  GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA  257
Qy    264  CAGCCTGAGAGCCGAGGACACACGGCTGTGTACTACTGTGCGAGAGATTCTAGATACAGTAA  323
Db    258  CAGCCTGAGAGCCGAGGACACGGCTGTGTTTATTACTGTGCGAGA------------  300
Qy    324  TTTCCTCCGTTGGGTTCGGAGGCGACGGCTCTGGGGCCAAGGGACCACGGTCAT  383
Db    301  -TCCAGTATTACGATTTTTGGTGTGGCGTATGGACGTCTCGGGGCCAAGGGCACCCTGGTCAC  359
Qy    384  CGTCTCCTCA  393
Db    360  CGTCTCCTCA  369
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RESULT 12
PCT-US03-02612-6
; Sequence 6, Application PC/TUS0302612
; GENERAL INFORMATION:
;   APPLICANT: Egea Biosciences, Inc.
;   APPLICANT: Evans, Glen A.
;   TITLE OF INVENTION: Methods For Creating Recombination
;   TITLE OF INVENTION: Products Between Nucleotide Sequences
;   FILE REFERENCE: FP-EA 5505
;   CURRENT APPLICATION NUMBER: PCT/US03/02612
;   CURRENT FILING DATE: 2003-01-29
;   PRIOR APPLICATION NUMBER: US 10/062,188
;   PRIOR FILING DATE: 2002-01-30
;   NUMBER OF SEQ ID NOS: 231
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 819
;   TYPE: DNA

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)...(777)
PCT-US03-02612-6

Query Match     69.08;    Score 271.2;  DB 1;   Length 819;
Best Local Similarity     86.2%;   Pred. No. 5.2e-69;
Matches  319;  Conservative  0;  Mismatches  33;  Indels  18;  Gaps  1;

Qy    24 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    18 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 77

Qy    84 CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG 143
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    78 CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG 137

Qy   144 GCTGGAGTGGGTCATCATTAGTAATAGTAATAACTTACATATAATACTACGGCAGT 203
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   138 GCTGGAGTGGGTCTCATCCATTAGTAGTAGTTACATATAATACTACGGCAGACTTGT 197

Qy   204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   198 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 257

Qy   264 CAGCCTGAGAGCCGAGGACACACGGCTGTGTACTACTGTGCGAGAGATTCTAGATACAGTAA 323
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   258 CAGCCTGAGAGCCGAGGACACACGGCTGTTTATTACTGTGCGAGA----------- 300

Qy   324 TTTCCTCCGTTGGGGTTCGGGGACGACGTATGGACGTCTCTGGGGCCCAAGGGACCACGGTCAT 383
         |||    |  |||||||        |||                  ||| ||||  |||||
Db   301 -TCCAGTATTACGATTTTTGGTGGGCCGGTATGGACGTCTCTGGGGCGAGGAGCACCCTGGGTCAC 359

Qy   384 CGTCTCCTCA 393
         ||||||||||
Db   360 CGTCTCCTCA 369
```

```
RESULT 13
PCT-US03-02612-6
; Sequence 6, Application PC/TUS0302612
; GENERAL INFORMATION:
;   APPLICANT: Egea Biosciences, Inc.
;   APPLICANT: Evans, Glen A.
;   TITLE OF INVENTION: Methods For Creating Recombination
;   TITLE OF INVENTION: Products Between Nucleotide Sequences
;   FILE REFERENCE: FP-EA 5505
;   CURRENT APPLICATION NUMBER: PCT/US03/02612
;   CURRENT FILING DATE: 2003-01-29
;   PRIOR APPLICATION NUMBER: US 10/062,188
;   PRIOR FILING DATE: 2002-01-30
;   NUMBER OF SEQ ID NOS: 231
;   SOFTWARE: FastSEQ for Windows Version 4.0
;
SEQ ID NO 6
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)...(777)
PCT-US03-02612-6

Query Match     69.08;    Score 271.2;  DB 2;   Length 819;
Best Local Similarity     86.2%;   Pred. No. 5.2e-69;
Matches  319;  Conservative  0;  Mismatches  33;  Indels  18;  Gaps  1;

Qy    24 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    18 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 77
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    84 CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG 143
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    78 CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG 137

Qy   144 GCTGGAGTGGGTCTCATCCATTAGTAATAGTAATAACTTACATATAATACTACCGACAGT 203
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   138 GCTGGAGTGGGTCTCATCCATTAGTAGTAGTTACATATAATACTACCGACAGACTTCGT 197

Qy   204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   198 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 257

Qy   264 CAGCCTGAGAGCCGAGGACACACGGCTGTGTACTACTGTGCGAGAGATTCTAGATACAGTAA 323
         ||||||||||||||||||||||||||||||||||||||||
Db   258 CAGCCTGAGAGCCGAGGACACACGGCTGTTTATTACTGTGCGAGA----------- 300

Qy   324 TTTCCTCCGTTGGGGTTCGGGGACGACGTATGGACGTCTCTGGGGCCCAAGGGACCACGGTCAT 383
         |||    |  |||||||        |||                  ||| ||||  |||||
Db   301 -TCCAGTATTACGATTTTTGGTGGGCCGGTATGGACGTCTCTGGGGCGAGGAGCACCCTGGGTCAC 359

Qy   384 CGTCTCCTCA 393
         ||||||||||
Db   360 CGTCTCCTCA 369
```

```
RESULT 14
US-10-062-188-6
; Sequence 6, Application US/10062188
; GENERAL INFORMATION:
;   APPLICANT: Evans, Glen A.
;   TITLE OF INVENTION: Methods For Creating Recombination
;   TITLE OF INVENTION: Products Between Nucleotide Sequences
;   FILE REFERENCE: P-EA 5008
;   CURRENT APPLICATION NUMBER: US/10/062,188
;   CURRENT FILING DATE: 2001-01-31
;   NUMBER OF SEQ ID NOS: 231
;   SOFTWARE: FastSEQ for Windows Version 4.0
;
SEQ ID NO 6
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)...(777)
US-10-062-188-6

Query Match     69.08;    Score 271.2;  DB 45;  Length 819;
Best Local Similarity     86.2%;   Pred. No. 5.2e-69;
Matches  319;  Conservative  0;  Mismatches  33;  Indels  18;  Gaps  1;

Qy    24 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    18 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 77

Qy    84 CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG 143
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    78 CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG 137

Qy   144 GCTGGAGTGGGTCTCATCCATTAGTAATAGTAATAACTTACATATAATACTACCGACAGT 203
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   138 GCTGGAGTGGGTCTCATCCATTAGTAGTAGTTACATATAATACTACCGACAGACTTCGT 197

Qy   204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   198 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 257

Qy   264 CAGCCTGAGAGCCGAGGACACACGGCTGTGTACTACTGTGCGAGAGATTCTAGATACAGTAA 323
         ||||||||||||||||||||||||||||||||||||||||
Db   258 CAGCCTGAGAGCCGAGGACACACGGCTGTTTATTACTGTGCGAGA----------- 300

Qy   324 TTTCCTCCGTTGGGGTTCGGGGACGACGTATGGACGTCTCTGGGGCCCAAGGGACCACGGTCAT 383
         |||    |  |||||||        |||                  ||| ||||  |||||
Db   301 -TCCAGTATTACGATTTTTGGTGGGCCGGTATGGACGTCTCTGGGGCGAGGAGCACCCTGGGTCAC 359

Qy   384 CGTCTCCTCA 393
         ||||||||||
Db   360 CGTCTCCTCA 369
```

```
Qy   324  TTTCCTCCGTTGGGTTCGGAGGACGGGTATGGACGTCTGGGGCGTCGGGGCCCAAGGGACCACGGTCAT  383
          |  |  |   ||  ||  ||||||||||||||||||||||||  || ||| |||||  |||||
Db   301  -TCCAGTATTACGATTTTTGGTGGCGGTATGGACGTCTGGGCGCAGAGGCACCCTGGTCAC  359

Qy   384  CGTCTCCTCA  393
          |||||||||
Db   360  CGTCTCCTCA  369
```

RESULT 15
US-10-172-118-198
; Sequence 198, Application US/10172118
; GENERAL INFORMATION:
;   APPLICANT: Dai, Hongyue
;   APPLICANT: He, Yudong
;   APPLICANT: Linsley, Peter
;   APPLICANT: Mao, Mao
;   APPLICANT: Roberts, Chris
;   APPLICANT: Van 't Veer, Laura
;   APPLICANT: Van de Vijver, Marc
;   APPLICANT: Bernards, Rene
;   TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
;   FILE REFERENCE: 9301-175-999
;   CURRENT APPLICATION NUMBER: US/10/172,118
;   CURRENT FILING DATE: 2002-06-14
;   PRIOR APPLICATION NUMBER: 60/380,770
;   PRIOR FILING DATE: 2002-05-14
;   NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 198
;   LENGTH: 819
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: AJ225092
;   DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-198

Query Match   69.0%; Score 271.2; DB 47; Length 819;
Best Local Similarity   86.2%; Pred. No. 5.2e-69;
Matches 319; Conservative   0; Mismatches   33; Indels   18; Gaps   1;

```
Qy    24  GGTGGAGTCTGGGGGAGGGCCTGGTCAAGCCTGGGGGGGGGGGTCCCTGAGACTCTCCTGTGCAGC   83
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    18  GGTGGAGTCTGGGGGAGGGCCTGGTCAAGCCTGGGGGGGGGGGTCCCTGAGACTCTCCTGTGCAGC   77

Qy    84  CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG  143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    78  CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG  137

Qy   144  GCTGGAGTGGGTCTCATCCATTAGTAATAGTTACATTATTACTACGGACGGCAGT  203
          ||||||||||||||||||||||||||||||||  ||||||||||||||||| ||
Db   138  GCTGGAGTGGGTCTCATCCATTAGTAGTAGTTACATATTACTACGGACTTCGT  197

Qy   204  GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA  263
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   198  GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA  257

Qy   264  CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGA------------  323
          ||||||||||||||||||||||||||||||||| || |||
Db   258  CAGCCTGAGAGCCGAGGACACGGCTGTTTATTACTGTGCGAGA------------  300

Qy   324  TTTCCTCCGTTGGGTTCGGAGGACGGGTATGGACGTCTGGGGCGTCGGGGCCCAAGGGACCACGGTCAT  383
          |  |  |   ||  ||  |||||||||||||||||||||  || ||| |||||  |||||
Db   301  -TCCAGTATTACGATTTTTGGTGGCGGTATGGACGTCTGGGCGCAGAGGCACCCTGGTCAC  359

Qy   384  CGTCTCCTCA  393
          |||||||||
Db   360  CGTCTCCTCA  369
```

; GENERAL INFORMATION:
;   APPLICANT: Dai, Hongyue
;   APPLICANT: He, Yudong
;   APPLICANT: Linsley, Peter S.
;   APPLICANT: Mao, Mao
;   APPLICANT: Roberts, Christopher J.
;   APPLICANT: Van 't Veer, Laura Johanna
;   APPLICANT: Bernards, Rene
;   APPLICANT: Van de Vijver, Marc J.
;   TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
;   FILE REFERENCE: 9301-188-999
;   CURRENT APPLICATION NUMBER: US/10/342,887
;   CURRENT FILING DATE: 2003-01-15
;   PRIOR APPLICATION NUMBER: 60/298,918
;   PRIOR FILING DATE: 2001-06-18
;   PRIOR APPLICATION NUMBER: 60/380,710
;   PRIOR FILING DATE: 2002-05-14
;   PRIOR APPLICATION NUMBER: 10/172,118
;   PRIOR FILING DATE: 2002-06-14
;   NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 198
;   LENGTH: 819
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-342-887-198

Query Match   69.0%; Score 271.2; DB 50; Length 819;
Best Local Similarity   86.2%; Pred. No. 5.2e-69;
Matches 319; Conservative   0; Mismatches   33; Indels   18; Gaps   1;

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Qy    24  GGTGGAGTCTGGGGGAGGGCCTGGTCAAGCCTGGGGGGGGGGGTCCCTGAGACTCTCCTGTGCAGC   83
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    18  GGTGGAGTCTGGGGGAGGGCCTGGTCAAGCCTGGGGGGGGGGGTCCCTGAGACTCTCCTGTGCAGC   77

Qy    84  CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG  143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    78  CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG  137

Qy   144  GCTGGAGTGGGTCTCATCCATTAGTAATAGTTACATTATTACTACGGACGGCAGT  203
          ||||||||||||||||||||||||||||||  ||||||||||||||||| ||
Db   138  GCTGGAGTGGGTCTCATCCATTAGTAGTAGTTACATATTACTACGGACTTCGT  197

Qy   204  GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA  263
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   198  GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA  257

Qy   264  CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGA------------  323
          ||||||||||||||||||||||||||||||||| || |||
Db   258  CAGCCTGAGAGCCGAGGACACGGCTGTTTATTACTGTGCGAGA------------  300

Qy   324  TTTCCTCCGTTGGGTTCGGAGGACGGGTATGGACGTCTGGGGCGTCGGGGCCCAAGGGACCACGGTCAT  383
          |  |  |   ||  ||  |||||||||||||||||||||  || ||| |||||  |||||
Db   301  -TCCAGTATTACGATTTTTGGTGGCGGTATGGACGTCTGGGCGCAGAGGCACCCTGGTCAC  359

Qy   384  CGTCTCCTCA  393
          |||||||||
Db   360  CGTCTCCTCA  369
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RESULT 17
US-60-474-850-84
; Sequence 84, Application US/60474850
; GENERAL INFORMATION:
;   APPLICANT: Wohlgemuth, Jay
;   APPLICANT: Ly, Ngoc
;   APPLICANT: Prentice, James
;   TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
;   TITLE OF INVENTION: RENAL TRANSPLANT REJECTION
;   FILE REFERENCE: 506613000700
;   CURRENT APPLICATION NUMBER: US/60/474,850
;   CURRENT FILING DATE: 2003-05-30
;   NUMBER OF SEQ ID NOS: 552
;   SOFTWARE: PatentIn version 3.1

RESULT 16
US-10-342-887-198
; Sequence 198, Application US/10342887

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; SEQ ID NO 84
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-474-850-84

Query Match      69.0%;  Score 271.2;  DB 102;  Length 819;
Best Local Similarity   86.2%;  Pred. No. 5.2e-69;
Matches 319;  Conservative  0;  Mismatches 33;  Indels 18;  Gaps 1;

Qy    24 GGTGGGAGTCTGGGGAGGACGCCTGGTCAGAGCCTGAGACTCTCCTGTGCAGC 83
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    18 GGTGGGAGTCTGGGGAGGACGCCTGGTCAGAGCCTGAGACTCTCCTGTGCAGC 77

Qy    84 CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGGAAGG 143
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    78 CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGGAAGG 137

Qy   144 GCTGGAGTGGGTGGGGTCTCATCCATTAGTAATAGTTACATAATACTACGCAGACGCAGT 203
         ||||||||||||||||||||||||||||||||||||||||||||| || || ||||||
Db   138 GCTGGAGTGGGGTTCTCATCCATTAGTAGTAGTTACATATACTACGCAGACTTCGT 197

Qy   204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   198 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 257

Qy   264 CAGCCTGAGAGCCGAGGACACGGCTGTGTACTACTGTGCGGAGAGATTCTAGATACAGTAA 323
         |||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   258 CAGCCTGAGAGCCGAGGACACGGCTGTTTATTTACTGTGCCGAGA------- 300

Qy   324 TTTCCTCCGTTGGGTTCGGGGAGGGACGGTATTGGACGCACAGGTCAT 383
         || | || | |||||||||||||||||||||| | || ||||||
Db   301 -TCCAGTATTACGATTTTTGGTGGCGGTATTGGACGCTCGGGGGGCAGAGGGCACCCTGGTCAC 359

Qy   384 CGTCTCCTCA 393
         ||||||||||
Db   360 CGTCTCCTCA 369
```

```
RESULT 18
PCT-US03-00398-55
Sequence 55, Application PC/TUS0300398
; GENERAL INFORMATION:
; APPLICANT: ABGENIX, INC.
; APPLICANT: CORVALAN, Jose, R.F.
; APPLICANT: JIA, Xiao-Chi
; APPLICANT: FENG, Xiao
; APPLICANT: YANG, Xiao-Dong
; APPLICANT: CHEN, Francine
; APPLICANT: GAZIT, Gadi
; APPLICANT: WEBER, Richard
; APPLICANT: BEZABEH, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES THEREOF
; FILE REFERENCE: ABGENIX.051VPC
; CURRENT APPLICATION NUMBER: PCT/US03/00398
; CURRENT FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 379
; TYPE: DNA
; ORGANISM: homo sapiens
PCT-US03-00398-55

Query Match      68.9%;  Score 270.8;  DB 1;  Length 379;
Best Local Similarity   85.1%;  Pred. No. 5.4e-69;
Matches 315;  Conservative  0;  Mismatches 52;  Indels 3;  Gaps 1;

Qy    24 GGTGGGAGTCTGGGGAGGACGCCTGGTCAGAGCCTGAGACTCTCCTGTGCAGC 83
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    12 GGTGGGAGTCTGGGGAGGACCTGGTCAAGCCTGGGGAGGTCCCTGAGACTCTCCTGTGCAGC 71

Qy    84 CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGGAAGG 143
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    72 CTCTGGATTCACCTTCAGAGACCTATAGCTAGCATGAGCATGCACTGGGTCCGCCAGGGAAGG 131

Qy   144 GCTGGAGTGGGTGGGGTCTCATCCATTAGTAATAGTTACATAATACTACGCAGACGCAGT 203
         |||||||||||||||||||||||||||| ||| || || ||||||||
Db   132 GCTGGAGTGGGTGGGGTCTCATCCATTAGTAGTAGTTACATATACTACGCAGACTTCAGT 191

Qy   204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   192 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 251

Qy   264 CAGCCTGAGAGCCGAGGACACGGCTGTGTACTACTGTGCGGAGAGATTCTAGATACAGTAA 323
         ||||||||||||||||||||||||||||| ||||||| | |||||||||
Db   252 CAGCCTGAGAGCCGAGGACACGGCTGTATATTACTGTGCGAGAGAACTCAGTGTATTGCAATGAA 308

Qy   324 TTTCCTCCGTTGGGTTCGGGGAGGGACGGTATTGGACGCACAGGTCAT 383
         || | || | ||||||||||||||||||| | | ||||||
Db   309 GTTTGGGGGGAATTATCGCCTCCGTTCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCAC 368

Qy   384 CGTCTCCTCA 393
         ||||||||||
Db   369 CGTCTCCTCA 378
```

```
RESULT 19
PCT-US03-00398-55
Sequence 55, Application PC/TUS0300398
; GENERAL INFORMATION:
; APPLICANT: ABGENIX, INC.
; APPLICANT: CORVALAN, Jose, R.F.
; APPLICANT: JIA, Xiao-Chi
; APPLICANT: FENG, Xiao
; APPLICANT: YANG, Xiao-Dong
; APPLICANT: CHEN, Francine
; APPLICANT: GAZIT, Gadi
; APPLICANT: WEBER, Richard
; APPLICANT: BEZABEH, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES THEREOF
; FILE REFERENCE: ABGENIX.051VPC
; CURRENT APPLICATION NUMBER: PCT/US03/00398
; CURRENT FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 379
; TYPE: DNA
; ORGANISM: homo sapiens
PCT-US03-00398-55

Query Match      68.9%;  Score 270.8;  DB 2;  Length 379;
Best Local Similarity   85.1%;  Pred. No. 5.4e-69;
Matches 315;  Conservative  0;  Mismatches 52;  Indels 3;  Gaps 1;

Qy    24 GGTGGGAGTCTGGGGAGGACGCCTGGTCAGAGCCTGAGACTCTCCTGTGCAGC 83
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    12 GGTGGGAGTCTGGGGAGGACCTGGTCAAGCCTGGGGAGGTCCCTGAGACTCTCCTGTGCAGC 71

Qy    84 CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGGAAGG 143
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    72 CTCTGGATTCACCTTCAGAGACCTATAGCTAGCATGAGCATGCACTGGGTCCGCCAGGGAAGG 131

Qy   144 GCTGGAGTGGGTGGGGTCTCATCCATTAGTAATAGTTACATAATACTACGCAGACGCAGT 203
         |||||||||||||||||||||||||||| ||| || || ||||||||
Db   132 GCTGGAGTGGGTGGGGTCTCATCCATTAGTAGTAGTTACATATACTACGCAGACTTCAGT 191

Qy   204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   192 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 251

Qy   264 CAGCCTGAGAGCCGAGGACACGGCTGTGTACTACTGTGCGGAGAGATTCTAGATACAGTAA 323
         ||||||||||||||||||||||||||||| ||||||| | |||||||||
Db   252 CAGCCTGAGAGCCGAGGACACGGCTGTATATTACTGTGCGAGAGATATTA---TGATTAC 308

Qy   324 TTTCCTCCGTTGGGTTCGGGGAGGGACGGTATTGGACGCACAGGTCAT 383
         || | || | ||||||||||||||||||| | | ||||||
Db   309 GTTTGGGGGGAATTATCGCCTCCGTTCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCAC 368

Qy   384 CGTCTCCTCA 393
         ||||||||||
Db   369 CGTCTCCTCA 378
```

```
Qy    324  TTTCCTCCGTTGGGTTCGGGAGCGACGGTATGACGTCTGGGGCCCAAGGGACCACGGTCAT  383
           | ||                 | || ||||  |||  |||||||||||||||||||||||||||
Db    309  GTTTGGGGGAATTATCGCCTCGTTCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCAC  368

Qy    384  CGTCTCCTCA  393
           ||||||||||
Db    369  CGTCTCCTCA  378
```

RESULT 20
US-1-041-860-55
; Sequence 55, Application US/10041860
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 55
;   LENGTH: 379
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-041-860-55

Query Match   68.9%; Score 270.8; DB 44;   Length 379;
Best Local Similarity 85.1%; Pred. No. 5.4e-69;
Matches 315; Conservative 0; Mismatches 52; Indels 3; Gaps 1;

```
Qy     24  GGTGGAGTCTGGGGGAGGCCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTCCAGC   83
           |||||||||  |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     12  GGTGGAGTCTGGGGGAGGCCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCCAGC   71

Qy     84  CTCTGGATTCACCTTCAGTAGCTATATAGCCATCGCCACTCGGGTCCGCCAGGGTCCAGGGAAGGG  143
           ||||||||||||  |  | |||||||| ||||| || ||||||||||||||||||||||||||||||
Db     72  CTCTGGATTCAACTTCAGAAACCTTATAACATGAACTGGGTCCGCCAGGCTCCAGGGAAGGG  131

Qy    144  GCTGGAGTGGGGTGCTCATCCCATTAGTAATGATAGTTAATACTTACAATATACTTACCGCAGACGACCAGT  203
           ||||||||| |||| |||||||||| ||||||||| |||  |||| ||||||||||||||||||||  |||
Db    132  GCTGGAGTGGGGTCTCATCCATTCATTAGTAGTAGTAGTAACATATACTTACCGGAGACTCAGT  191

Qy    204  GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA  263
           | |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db    192  GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA  251

Qy    264  CAGCCTGAGAGCCGAGGACACACGGCTGTGTACTACTGTGCGAGAGATTCTAGATACAGTAA  323
           |||||||||||||||||  |||||||||| ||| |||||||||||||||||  ||  || ||
Db    252  CAGCCTGAGAGCCGAGGACACGGCTGTATATTACTGTGCGAGAGATTATTA---TGATTAC  308

Qy    324  TTTCCTCCGTTGGGTTCGGGAGCGACGGTATGGACGTCTGGGGCCCAAGGGACCACGGTCAT  383
           |||                    |  |||| ||||||||||||||||||||||||||||||
Db    309  GTTTGGGGGAATTATCGCCTCGTTCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCAC  368

Qy    384  CGTCTCCTCA  393
           ||||||||||
Db    369  CGTCTCCTCA  378
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Job time : 3361 secs

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                                    GenCore version 5.1.6

                                    Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:            September 24, 2003, 03:27:44 ; Search time 864 Seconds
                                                  (without alignments)
                                                  554.003 Million cell updates/sec

Title:
Perfect score:     393
Sequence:          1 gaggtgcagctgctcgagtc.........ccacggtcatcgtctcctca 393

Scoring table:     IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched:          960753 seqs, 608980626 residues

Total number of hits satisfying chosen parameters:    1921506

Post-processing:   Minimum Match 0%
                   Maximum Match 100%
                   Listing first 60 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database :         Pending_Patents_NA_New:*
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                   2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
                   3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
                   4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
                   5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
                   6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
                   7: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result NO.	Score	% Query Match	Length	DB	ID	Description
1	273.6	69.6	369	1	PCT-US03-21304-3	Sequence 3, Appli
2	248	63.1	747	1	PCT-US03-25457-65	Sequence 65, Appl
3	247.6	63.0	741	1	PCT-US03-23826-46	Sequence 46, Appl
4	244.6	62.2	469219	7	US-60-495-114-16704	Sequence 16704, A
5	239.8	61.0	436	1	PCT-US03-26222-145	Sequence 145, App
6	236.8	60.3	510	1	US-10-469-304-16	Sequence 16, Appl
7	233.4	59.4	360	1	PCT-US02-34154-19	Sequence 19, Appl
8	233.4	59.4	360	1	US-10-456-092A-19	Sequence 19, Appl
9	233.4	59.4	1430	1	PCT-US02-26588-1	Sequence 1, Appl
10	232.8	59.2	357	1	PCT-US02-34154-20	Sequence 20, Appl
11	232.8	59.2	357	1	US-10-456-092A-20	Sequence 20, Appl
12	231.6	58.9	393	1	PCT-US03-15937-52	Sequence 52, Appl
13	231.2	58.8	867	5	US-09-194-164-16	Sequence 16, Appl
14	231.2	58.8	918	5	US-09-194-164-13	Sequence 13, Appl
15	231.2	58.8	918	5	US-09-194-164-15	Sequence 15, Appl
16	230	58.5	372	6	US-10-031-722A-1	Sequence 1, Appli
17	229.6	58.4	867	5	US-09-194-164-18	Sequence 18, Appl
18	227	57.8	360	5	US-09-849-390-121	Sequence 121, App
19	226	57.5	366	6	US-10-031-722A-5	Sequence 5, Appli
20	225.8	57.5	352	1	PCT-US03-25161-17	Sequence 17, Appl
21	225.6	57.4	417	6	US-10-656-769-9	Sequence 9, Appli
22	225.6	57.4	1395	6	US-10-656-769-21	Sequence 21, Appl
23	225.6	57.4	1398	6	US-10-656-769-23	Sequence 23, Appl
24	225.6	57.4	1407	6	US-10-656-769-19	Sequence 19, Appl
25	225.2	57.3	351	1	PCT-US03-21304-14	Sequence 4, Appl
26	224.4	57.1	908	6	US-10-375-356A-9	Sequence 9, Appli
27	224	57.0	366	6	US-10-031-722A-9	Sequence 9, Appli
28	224	57.0	903	6	US-10-375-356A-12	Sequence 12, Appl
29	224	57.0	913	6	US-10-375-356A-10	Sequence 10, Appl
30	223.6	56.9	351	1	PCT-US03-21304-5	Sequence 5, Appl
31	223.6	56.9	351	1	PCT-US03-21304-6	Sequence 6, Appl
32	222	56.5	351	1	PCT-US03-21304-7	Sequence 7, Appl
33	220.8	56.2	417	6	US-10-656-769-13	Sequence 13, Appl
34	220.8	56.2	1395	6	US-10-656-769-27	Sequence 27, Appl
35	220.8	56.2	1398	6	US-10-656-769-29	Sequence 29, Appl
36	220.8	56.2	1407	6	US-10-656-769-25	Sequence 25, Appl
37	220.4	56.1	351	6	US-10-656-769-25	Sequence 25, Appl
38	220.4	56.1	351	1	PCT-US03-21304-8	Sequence 8, Appl
39	219.4	55.8	1392	6	US-10-645-215-7	Sequence 7, Appli
40	218.8	55.7	351	1	PCT-US03-21304-10	Sequence 10, Appl
41	217.2	55.3	369	1	PCT-US03-19333-25	Sequence 25, Appl
42	214.8	54.7	336	1	PCT-US03-21304-11	Sequence 11, Appl
43	213.6	54.4	345	1	PCT-US03-21304-15	Sequence 15, Appl
44	213	54.2	743	6	US-09-538-038A-2352	Sequence 2352, Ap
45	212.4	54.0	892	6	US-10-375-356A-11	Sequence 11, Appl
46	212	53.9	345	1	PCT-US03-21304-13	Sequence 13, Appl
47	211.6	53.8	411	1	PCT-US03-15937-54	Sequence 54, Appl
48	211	53.7	752	5	US-09-538-038A-2350	Sequence 2350, Ap
49	209.6	53.3	363	1	PCT-US03-22566-337	Sequence 337, App
50	209.6	53.3	1493	1	PCT-US03-18934-94	Sequence 94, Appl
51	209.2	53.1	345	1	PCT-US03-21304-12	Sequence 12, Appl
52	208.2	53.0	348	1	PCT-US03-10749A-13	Sequence 13, Appl
53	208.2	53.0	369	1	PCT-US02-30316-1	Sequence 1, Appli
54	208.2	53.0	1413	6	US-10-749A-37	Sequence 37, Appl
55	207.8	52.9	369	1	PCT-US03-19333-27	Sequence 27, Appl
56	207.2	52.7	358	1	PCT-US03-25161-73	Sequence 73, Appl
57	207.2	52.7	738	1	PCT-US03-19333-33	Sequence 33, Appl
58	205.6	52.3	345	1	PCT-US03-21304-14	Sequence 14, Appl
59	204.8	52.1	432	6	US-10-257-864A-66	Sequence 66, Appl
60	204.8	52.1	738	1	PCT-US03-19333-30	Sequence 30, Appl

ALIGNMENTS

```
RESULT 1
PCT-US03-21304-3

Sequence 3, Application PCT/US0321304

GENERAL INFORMATION:
 APPLICANT: Siegel, Donald L.
 TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
 TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF
 FILE REFERENCE: 053893-5050WO
 CURRENT APPLICATION NUMBER: PCT/US03/21304
 CURRENT FILING DATE: 2003-07-03
 PRIOR APPLICATION NUMBER: 60/394,356
 PRIOR FILING DATE: 2003-07-03
 PRIOR APPLICATION NUMBER: 60/411,694
 PRIOR FILING DATE: 2003-09-18
 NUMBER OF SEQ ID NOS: 153
 SOFTWARE: PatentIn version 3.2

 SEQ ID NO 3
   LENGTH: 369
   TYPE: DNA
   ORGANISM: Homo sapiens
PCT-US03-21304-3

Query Match             69.6%;  Score 273.6;  DB 1;  Length 369;
Best Local Similarity   86.2%;  Pred. No. 3e-75;
Matches    319;  Conservative     0;  Mismatches  39;  Indels  12;  Gaps     1;

Qy          24 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
               ||||||||| || |||||||||||||||||||||||||||||||||||||||||||||||
Db          12 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 71

Qy          84 CTCTGGATTCACCTTCAGTAGCTATAPGCACTGGGTCCGCCAGGGTCCAGGGAAGGG 143
               |||||||| ||||||||||||||| ||||||||||| |||||||||||||||||||||
Db          72 CTCTGGATTCACCTTCAGTAGCTATAGCATAGAACTGGGTCCGCCAGGCTCCAGGGAAGGG 131
```

RESULT 2
PCT-US03-25457-65
Sequence 65, Application PC/TUS0325457
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
        Receptors
FILE REFERENCE: PF550PCT2
CURRENT APPLICATION NUMBER: PCT/US03/25457
CURRENT FILING DATE: 2003-08-15
PRIOR APPLICATION NUMBER: 60/468,050
PRIOR FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: 60/425,730
PRIOR FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 60/403,382
PRIOR FILING DATE: 2002-08-15
NUMBER OF SEQ ID NOS: 70
SEQ ID NO 65
LENGTH: 747
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: DNA encoding T100SF07 scFv

PCT-US03-25457-65

Query Match   63.1%;   Score 248; DB 1; Length 747;
Best Local Similarity   82.0%;   Pred. No. 3.4e-67;
Matches   300; Conservative   0; Mismatches   60; Indels   6; Gaps   1;

RESULT 3
PCT-US03-23826-46
Sequence 46, Application PC/TUS0323826
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Antibodies Against C3a Receptor
FILE REFERENCE: PF588PCT
CURRENT APPLICATION NUMBER: PCT/US03/23826
CURRENT FILING DATE: 2003-07-31
PRIOR APPLICATION NUMBER: 60/400,057
PRIOR FILING DATE: 2002-08-02
NUMBER OF SEQ ID NOS: 50
SEQ ID NO 46
LENGTH: 741
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Polynucleotide encoding D18SG07 scFv

PCT-US03-23826-46

Query Match   63.0%;   Score 247.6; DB 1; Length 741;
Best Local Similarity   88.7%;   Pred. No. 4.6e-67;
Matches   268; Conservative   0; Mismatches   34; Indels   0; Gaps   0;

RESULT 4
US-60-495-114-16704
Sequence 16704, Application US/60495114
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL001480
CURRENT APPLICATION NUMBER: US/60/495,114
CURRENT FILING DATE: 2003-08-15
NUMBER OF SEQ ID NOS: 91238
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16704
LENGTH: 469219
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:

```
NAME/KEY: misc_feature
LOCATION: (1)...(469219)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-60-495-114-16704

Query Match     Best Local Similarity 85.9%;  Conservative 7;  Mismatches 36;  Indels 0;  Gaps 0;
Matches 262;    Score 244.6;  DB 7;  Length 469219;

Qy      4 GTGCAGTGACTGCAGTCTGGGGTGGAGTCTGGGGGAGGCCTGCTCACGCCTGGGGGTCC 63
            ||| ||  ||||||||||||||||||||||| ||||||  |||||||||:||||||||||
Db 100714 GTCCAGTGTCAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTTGGTCAAGCCTGGGGGGTCC 100773

Qy     64 CTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTC 123
            |||||||| || ||| ||| |||||||||||||||||||  |||| |||||| ||||||
Db 100774 CTGAGACTSTCTGTSCAGMCTCTGGATTCACCTTCAGTGACTTAC...CATGCACTGGGTC 100833

Qy    124 CGCCAGGGTCCAGGGAAGGGGCTGGAGTGGGTG 183
            |||||||||||||||||||| ||||||||||||
Db 100834 CCCCAGGGCTCCAGGGAAGGGGCTGGAGTGGGTTGGRTTTCATACATTAGTAGTRGTRACC 100893

Qy    184 ATATACTACGCAGACGAGTGAAGGGCCGATTCACCATTCCAGAGACAACGCCAAGAAC 243
            || | ||| |||||| ||||||||||||||||||||||| |||||||||||||||||
Db 100894 ATATACTACGCAGAGACTCTGTGAAGGGCCGATTCACCATYCCAGGGACAACGCCCAAGAAC 100953

Qy    244 TCACTGTATTCTGCAAATGAACACACCTGAGAGCCGAGCACACGCCGTGTCTACTACTGTGCG 303
            ||||||||||| |||||||||||:|||||||||||||||||||| |||||||||||||||
Db 100954 TCACTGTATCTCGCAAATGAACACACCTGAGAGCCGAGCACACGCCGTGTATTAÇTGTGTCG 101013

Qy    304 AGAGA 308
            |||||
Db 101014 AGAGA 101018
```

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RESULT 5
PCT-US03-26232-145
Sequence 145, Application PC/US0326232
GENERAL INFORMATION:
APPLICANT: ARGENIX, INC.
APPLICANT: GUDAS, Jean M.
APPLICANT: HAAK-FRENDSCHO, Mary
APPLICANT: FOORD, Orit
APPLICANT: LIANG, Meina L.
APPLICANT: AHLUWALIA, Kiran
APPLICANT: BHAKTA, Sunil
TITLE OF INVENTION: ANTIBODIES DIRECTED TO MONOCYTE
TITLE OF INVENTION: CHEMO-ATTRACTANT PROTEIN-1 (MCP-1) AND USES THEREOF
FILE REFERENCE: ARGENIX.091VPC
CURRENT APPLICATION NUMBER: PCT/US03/26232
CURRENT FILING DATE: 2003-08-19
PRIOR APPLICATION NUMBER: US 60/404,802
PRIOR FILING DATE: 2002-08-19
NUMBER OF SEQ ID NOS: 149
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 145
LENGTH: 436
TYPE: DNA
ORGANISM: Homosapien
PCT-US03-26232-145

Query Match     Best Local Similarity 81.0%;  Conservative 0;  Mismatches 52;  Indels 18;  Gaps 1;
Matches 299;    Score 239.8;  DB 1;  Length 436;

Qy     25 GTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCC 84
            ||||||| |||| ||||  ||||||||||||||||||||||||||||||||||||||||||
Db      1 GAGCAGTCGGGGAGGCGGTCCAGCCTGGGGAGTCTCCTGTGCAGACTCTCCTGTGCACG 60

Qy     85 TCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTTCAGGGAGGG 144
            |||||||||||||||||||||||||||| |||||||| ||||||||||
Db     61 TCTGGATTCACCTTCAGTAGCTATATGGCACTGGGTCCGCCAGGCTCCAGGGAAGGGG 120

Qy    145 CTGGAGTGGGTCTCATCCATTAGTAGTAATACTACGCAGACGCGAGTG 204
            ||||||||||||| |||| || |||||||||||||||||||||||||||
Db    121 CTGGAGTGGGTGGGCAGTTATATATGGTATGATGGAAGTAATAAATACTACGCCGTG 180
```

```
RESULT 6
US-10-469-304-16
Sequence 16, Application US/10469304
GENERAL INFORMATION:
APPLICANT: KIRIN BEER KABUSHIKI KAISHA
TITLE OF INVENTION: Anti HLA-DR antibody
FILE REFERENCE: PH-1646-PCT
CURRENT APPLICATION NUMBER: US/10/469,304
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: JP2001/317054
PRIOR FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 510
TYPE: DNA
ORGANISM: Homo sapiens
US-10-469-304-16

Query Match     Best Local Similarity 80.0%;  Conservative 0;  Mismatches 62;  Indels 12;  Gaps 1;
Matches 296;    Score 236.8;  DB 6;  Length 510;

Qy     24 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
            ||||||||| |||||| |||| ||||||||||||||||| ||||||||||||||||||||
Db     24 GTTGGAGTCTGGGGGAGGCTTGGTCACGCCTGGGGGGTCCCTGAGACTCTCCTGTGTCAGC 83

Qy     84 CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG 143
            ||||||||||||||||||||||||| || ||||||| |||||||||||||||||||||||
Db    147 CTCTGGATTCACCTTTAGCAGCTATAGCCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG 206

Qy    144 GCTGGAGTGGGTCTCATCCATTAGTAGTAATACTACTACACGAGACAGCGCAGT 203
            |||||||||||| |||||  ||  ||||| |||||||||||||||||||||||||
Db    267 GCTGGAGTGGGTCTCAGGTATTAGTTGGTTGGTGATAGCAATATTCGGCGAGACTCCGT 326

Qy    204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
            ||||||||||||||||||||||||||||||||||||||| ||| |||||||||||||||||
Db    327 GAAGGGCCGGTTCACCATCTCCAGAGACAACGCCAAGAACACGCTGTATCTGCAAATGAA 386

Qy    264 CAGCCTGAGAGCCGAGGACACGGCTGTGTACTACTGTGCGAGAGATTCTAGATACAGTAA 323
            |||||||||||||||||||||||||||||||||||| |||||||||||||| |||||| |
Db    387 CAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGAGATCATGGTTCGGGGAG 446
```

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RESULT 7

Query Match     Best Local Similarity 61.0%;  Conservative 0;  Pred. No. 1e-64;  Gaps 1;
Matches 299;    Score 244.6;  ...  Pred. No. 3.2e-65;

Db    121 CTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTACGCCGTG 180

Db    205 AAGGGCCGGATTCACCATCTCCAGAGACAACGCCAAGAACAGCCAAGAACAGCTCACTGTATCTGCAAATGAAC 264

Db    181 AAGGGCCGGATTCACCATCTCCAGAGACAACGGCTGTGTACTACTGTGTGCG 240

Db    265 AGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATAGCAGTGA 324

Db    241 AGCCTGAGACCGAGGACACGGCTGTGTATTACTGTGCGAGAGATTCTAGATACAGTAAT 300

Db    325 TTCCTCCGTTGGGGTTCGGGGACGGCGGTATGGACCTGGTATGGACGGGTCATC 384

Db    301 T-----------ACTACGGTATGGACGGGTCATC 342

Qy    385 GTCTCCTCA 393          Qy    343 GTCTCCTCA 351
          |||||||||                        |||||||||
Db    385 GTCTCCTCA 393          Db    343 GTCTCCTCA 351
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```
Db    324 TTTTCCTCCGTTGGGGTTCGGAGCGAGGAGTATGGACGGGTCAAGGGACCACGGTCAT 383
Db    447 TT-------------ATTATCCCTACTGGTTTGACTACTGGGGCCAGGGAACCCTGGTCAC 494

Qy    384 CGTCTCCTCA 393          Qy    495 CGTCTCCTCA 504
          ||||||||||                        ||||||||||
Db    384 CGTCTCCTCA 393          Db    495 CGTCTCCTCA 504
```

```
PCT-US02-34154-19
Sequence 19, Application PC/TUS0234154
; GENERAL INFORMATION:
; APPLICANT: Centocor Inc.
; APPLICANT: Scalon, Bernard J.
; TITLE OF INVENTION: RSV PROTEINS, ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0203PCT
; CURRENT APPLICATION NUMBER: PCT/US02/34154
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/336081
; PRIOR FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 19
; LENGTH: 360
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-34154-19

Query Match          59.4%;  Score 233.4;  DB 1;  Length 360;
Best Local Similarity  87.6%;  Pred. No. 9.4e-63;
Matches  255;  Conservative  0;  Mismatches  36;  Indels  0;  Gaps  0;

Qy   25 GTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCC   84
         |||||||||||||||||| |||||||  ||||||||||||||| ||||||||  ||||||||
Db   16 GAGGAGTCTGGGGGAGGCCTGGTCACGCCTGGGGGGTCCCTTAAGACTCTCGTGTGCAGCC  75

Qy   85 TCTGGATTCACCTTCAGTAGCTATAGCATGGACTGGGTCCGCCAGGCTCCAGGGAAGGGG  144
         ||||||  || |||| |||| ||| || || ||||||||||||||||||||||||||||||
Db   76 TCTGGAACCACCCTCAGTGGGTATTACACCATGGACTGGGTCCGCCAGGGTCCAGGGAAGGGG  135

Qy  145 CTGGAGTGGGTGGTCTCATCCATTAGTAATAGTAATAAATACTTACGAGCAGACGCCAGTG  204
         ||||||||||| |||||||||||||||||| |||||||||||||||||||||||||||
Db  136 CTGGAGTGGGTCTCATCCATTAGTAATAGTAATAAATACTTACGAGCAGACGCCAGTG  195

Qy  205 AAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAAC  264
         ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db  196 AAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTTTATCTGCAAATGAAC  255

Qy  265 AGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATTCTAGA           315
         |||||| ||||||||||||||||| |||| | ||||||| | |  |
Db  256 AGCCTGACAGCCGAGGACACGGCTGTCTATTATTGTGCGACCGCCCCCTATA          306
```

```
RESULT 8
US-10-456-092A-19
Sequence 19, Application US/10456092A
; GENERAL INFORMATION:
; APPLICANT: Centocor Inc.
; APPLICANT: Scalon, Bernard J.
; TITLE OF INVENTION: RSV PROTEINS, ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0203USNP
; CURRENT APPLICATION NUMBER: US/10/456,092A
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/336081
; PRIOR FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 19
; LENGTH: 360
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-456-092A-19

Query Match          87.6%;  Score 233.4;  DB 6;  Length 360;
Best Local Similarity  87.6%;  Pred. No. 9.4e-63;
Matches  255;  Conservative  0;  Mismatches  36;  Indels  0;  Gaps  0;

Qy   25 GTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCC   84
         |||||||||||||||||| |||||||  ||||||||||||||| ||||||||  ||||||||
Db   16 GAGGAGTCTGGGGGAGGCCTGGTCACGCCTGGGGGGTCCCTTAAGACTCTCGTGTGCAGCC  75

Qy   85 TCTGGATTCACCTTCAGTAGCTATAGCATGGACTGGGTCCGCCAGGCTCCAGGGAAGGGG  144
```

```
RESULT 9
PCT-US02-26584-1
Sequence 1, Application PC/TUS0226584
; GENERAL INFORMATION:
; APPLICANT: HOOPER, Craig
; APPLICANT: DIETZSCHOLD, Bernhard
; TITLE OF INVENTION: Recombinant Antibodies, and Compositions
               and Methods for Making Them
; FILE REFERENCE: 8321-110 PC
; CURRENT APPLICATION NUMBER: PCT/US02/26584
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/314,023
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1430
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-26584-1

Query Match          59.4%;  Score 233.4;  DB 1;  Length 1430;
Best Local Similarity  79.1%;  Pred. No. 1.5e-62;
Matches  292;  Conservative  0;  Mismatches  71;  Indels  6;  Gaps  1;

Qy   24 GGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC   83
         | ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db   72 GTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC  131

Qy   84 CTCTGGATTCACCTTCAGTAGCTATAGCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGG  143
         |||||||||||||||  || ||| ||||||||||||||||||||||||||||||||||||
Db  132 CTCTGGATTCACCTTTAGCAACTATGCCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGG  191

Qy  144 GCTGGAGTGGGTCTCATCCATTAGTAATAGTAATAAATACTTACACAGCAGACGCCAGT   203
         ||||||||||||||||  | |||||| ||||| |  ||| ||| || ||||| || ||
Db  192 GCTGGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTATGCAGACTCCGT  251

Qy  204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA  263
         |||||||||| ||||||||||||||||||  |||||||| || |||||||||||||||||
Db  252 GAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAA  311

Qy  264 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGA                 323
         ||||||||||||||||||||||||  ||| || ||||| | | ||
Db  312 CAGCCTGAGAGCCGAGGACACGGCCGTATTATTACTGTACTACTGTCCGAAAGATCAGAGGGTTACTAT  371

Qy  324 TTTCCTCCGTTGGGTTCGGACGCGGCGTATGGACGTCTGGGGCCAAGGGACCACGGTCAT  383
         |  || |||| ||  | ||| | | ||||| ||| |||||||||||||| ||||  ||||
Db  372 GATAGT------TGTACTTAATGGAGGCTTTGACTACTGGGGCCAGGGAACCCGGGTCAC  425

Qy  384 CGTCTCCTC  392
         |||||||||
Db  426 CGTCTCCTC  434
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RESULT 10
PCT-US02-34154-20
; Sequence 20, Application PC/TUS0234154
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; GENERAL INFORMATION:
;  APPLICANT: Centocor Inc.
;  APPLICANT: Scallon, Bernard J.
;  TITLE OF INVENTION: RSV PROTEINS, ANTIBODIES, COMPOSITIONS, METHODS AND USES
;  FILE REFERENCE: CEN0203PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/34154
;  CURRENT FILING DATE: 2003-06-16
;  PRIOR APPLICATION NUMBER: 60/336081
;  PRIOR FILING DATE: 2001-11-02
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: Patentin version 3.1
;
;  SEQ ID NO 20
;   LENGTH: 357
;   TYPE: DNA
;   ORGANISM: Homo sapiens
PCT-US02-34154-20

Query Match             59.28%;  Score 232.8;  DB 1;  Length 357;
Best Local Similarity   87.3%;   Pred. No. 1.4e-62;
Matches  255;  Conservative  0;  Mismatches  37;  Indels  0;  Gaps  0;

Qy     24 GGTGGAGTCTGGGGGAGGCCTTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
          | ||||||||||||||||||||||| ||||||| |||||| |||||||||||||||||||
Db     12 GCTCGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCGTGTGCAGC 71

Qy     84 CTCTGGATTCACCTTCAGTAGCTATAGCATGCATGCCTGGGTCCGCCAGGCTCCAGGGAAGGG 143
          |||||||  ||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db     72 CTCTGGAACCACCTCAGTGGCTATAGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG 131

Qy    144 GCTGGAGTGGGTCTCATCCATTAGTAATAGTAATACTTACATATACTACGCAGACGCAGT 203
          |||||||||||||| | |||  ||  |||||  | ||||||||||||||||||||||||
Db    132 GCTGGAGTGGGGTCTCATCCATTACTGGAGGGTAGCAACTTCATAAACTACTCAGT 191

Qy    204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCCCAAGAACTCACTGTATCTGCAAATGAA 263
          || ||||||||||||||||||||||||||  | ||| |  |||||||||||| ||||| ||
Db    192 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTTTATCTGCAAATGAA 251

Qy    264 CAGCCTGAGAGCCGAGGACACAGCCGTGTACTACTGTGCGAGAGATTCTAGA 315
          |||||||| |  ||||||||| || ||||||||||||||||||||||||||||
Db    252 CAGCCTGACAGCCGAGGACACGGCCGTGTCTATTATTGTGCGAGAGATTCTAGA 303
```

```
RESULT 11
US-10-456-092A-20
; Sequence 20, Application US/10456092A
; GENERAL INFORMATION:
;  APPLICANT: Centocor Inc.
;  APPLICANT: Scallon, Bernard J.
;  TITLE OF INVENTION: RSV PROTEINS, ANTIBODIES, COMPOSITIONS, METHODS AND USES
;  FILE REFERENCE: CEN0203USNP
;  CURRENT APPLICATION NUMBER: US/10/456,092A
;  CURRENT FILING DATE: 2003-06-06
;  PRIOR APPLICATION NUMBER: 60/336081
;  PRIOR FILING DATE: 2001-11-02
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: Patentin version 3.1
;
;  SEQ ID NO 20
;   LENGTH: 357
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-456-092A-20

Query Match             59.28%;  Score 232.8;  DB 6;  Length 357;
Best Local Similarity   87.3%;   Pred. No. 1.4e-62;
Matches  255;  Conservative  0;  Mismatches  37;  Indels  0;  Gaps  0;

Qy     24 GGTGGAGTCTGGGGGAGGCCTTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
          | ||||||||||||||||||||||| ||||||| |||||| |||||||||||||||||||
Db     12 GCTCGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCGTGTGCAGC 71

Qy     84 CTCTGGATTCACCTTCAGTAGCTATAGCATGCATGCCTGGGTCCGCCAGGCTCCAGGGAAGGG 143
          |||||||  |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     72 CTCTGGAACCACCTCAGTGGCTATAGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG 131
```

```
RESULT 12
PCT-US03-15937-52
; Sequence 52, Application PC/TUS0315937
; GENERAL INFORMATION:
;  APPLICANT: Hematech, LLC et al.
;  TITLE OF INVENTION: Transgenic Ungulates Capable of Human
;  TITLE OF INVENTION: Antibody Production
;  FILE REFERENCE: 5019/012W02
;  CURRENT APPLICATION NUMBER: PCT/US03/15937
;  CURRENT FILING DATE: 2003-07-28
;  PRIOR APPLICATION NUMBER: US 60/381,531
;  PRIOR FILING DATE: 2002-05-17
;  PRIOR APPLICATION NUMBER: US 60/425,056
;  PRIOR FILING DATE: 2002-11-08
;  NUMBER OF SEQ ID NOS: 94
;  SOFTWARE: FastSEQ for Windows Version 4.0
;
;  SEQ ID NO 52
;   LENGTH: 393
;   TYPE: DNA
;   ORGANISM: Bovine
PCT-US03-15937-52

Query Match             58.9%;   Score 231.6;  DB 1;  Length 393;
Best Local Similarity   91.1%;   Pred. No. 3.5e-62;
Matches  246;  Conservative  0;  Mismatches  24;  Indels  0;  Gaps  0;

Qy     37 GGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCCTGGATTCACC 96
          ||||| | | | ||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GGAGGCCTTTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCAGCCTGGATTCACC 60

Qy     97 TTCAGTAGCTATAGCAATGCACTGGGTCCGCGCCAGGGCTCCAGGGAAGGGGCTGGAGTGGGTC 156
          ||||| |  |||||||||| |||||| |||| | || |||  ||||| |||||||||||||||
Db     61 TTCAGTGACTACTACATGAGCTGGGATCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTT 120

Qy    157 TCATCCATTAGTAATAGTAATTACTTACATATACTACGCAGACGCAGTGAAGGGCCGATTC 216
          |||| | || ||  |  | ||  || ||||||| |||||||||||||||||||||||||||
Db    121 TCATCACATTAGTAGTGGTAGTACCATATACTACGCAGACTCTGAAGGGCCGATTC 180

Qy    217 ACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAACAGCCTGAGAGCC 276
          ||||||||||||||||| ||| ||||||||||| || |||| ||||| |||||| |||||
Db    181 ACCATCTCCAGGGACAACGCCAAGAACTCACTGTATCTGCAAATGAACAGCCTGAGAGCC 240

Qy    277 GAGCACACGGCCGTGTGTTACTACTGTGCGAGA 306
          || | ||| || ||||| || ||||||||||||
Db    241 GAGGACACGGCTGTGTATTACTGTGCGAGA 270
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```
RESULT 13
US-09-194-164-16
; Sequence 16, Application US/09194164
; GENERAL INFORMATION:
;  APPLICANT: Dan, Michael D.
;                    Maiti, Pradip K.
;                    Kaplan, Howard A.
;  TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT
;  SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING T
;  FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
;  DETECTION OF CANCERS
;  NUMBER OF SEQUENCES: 18
```

RESULT 14

Left record

CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/194,164
FILING DATE: 09-Apr-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/657,449
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 867 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: join(1..855, 862..867)
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-194-164-16

Query Match   58.8%; Score 231.2; DB 5; Length 867;
Best Local Similarity   78.6%; Pred. No. 6.1e-62;
Matches 291; Conservative   0; Mismatches 73; Indels 6; Gaps 1;

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Qy    24 GGTGGGAGTCTGGGGGAGGAGGCCCTGGCTCAAGCCTGGGGGGGTCCCTGAGACTCCTGTGCAGC 83
          |||||||||| || |||||| || | |  || ||||| ||| ||||||||||||| ||||||||
Db   438 GGTGGGAGTTCTGGGGGAGGCCTGGGTCCAGCCTCGGGAGGTCCCTGAGACTCTCCGTGTGCAGC 497

Qy    84 CTCTGGGATTCACCTTCAGTAGCTATAGCAATGGCACTGGGGTCCGCCAGGGTCCAGGGAAGGG 143
          |||||||||| ||||||| | || ||| |||| |||||||||||| |||||| |||||| ||||
Db   498 CTCTGGGATTCCCCTTCAGAAGCTTTGCTATTGCACTGGGGTCCCGCCAGGGCTCAGGGCAAGGG 557

Qy   144 GCTGGAGTGGGGTCTCATCCATTAGTAATAGTAATAACTTTACATATAATTACACGACGAGCCGT 203
          |||||||||||| |    |  ||||| || | || |  ||| || | |  |||  |  |    ||
Db   558 GCTGGAGTGGGTGGCAGTTATATCATATGAAGCACTAAATACTACCGCAGACTCCGT 617

Qy   204 GAAGGGCCGAGTTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAAATGAA 263
          ||||| |||| ||||||||| |||||| || ||| ||||| |||||| |||| ||||||||
Db   618 GAAGGGCCGATTCACCATCTCCAGAGACACTTCCAAGAACACGGTGTATCTAAGATACAGTAA 677

Qy   264 CAGCCTGAGAGCCGAGGACACACGGCTGTGTATTACTACTGCGCAGAGAGACGGCAGT 323
          ||||||||||| ||| |  ||| ||| || |||||||| ||  |||  |||   || 
Db   678 CAGCCTGAGAACTGAGGACACGGCTGTCTATTACTGTGCCGAGGAT------CAGAGGCT 731

Qy   324 TTTCCTCCGTTGGGTTCGGAGCGACGGGTATGGACGTCTCGGGCCAAGGGACCACGGTCAT 383
          |||| || |||| |  |||   | ||||| | |||  |  |||||||||||||||||| |
Db   732 GTTGGGGTGACTATGACCACTACGGTTTGGACGTCTCTGGGCAAAGGGACCACGGTCAC 791

Qy   384 CGTCTCCTCA 393
          ||||||||||
Db   792 CGTCTCCTCA 801
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Right record

US-09-194-164-13
Sequence 13, Application US/09194164
GENERAL INFORMATION:
APPLICANT: Dan, Michael D.
   Malti, Pradip K.
   Kaplan, Howard A.
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING T
   FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
   DETECTION OF CANCERS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/194,164
FILING DATE: 09-Apr-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/657,449
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: join(1..906, 913..918)
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-194-164-13

Query Match   58.8%; Score 231.2; DB 5; Length 918;
Best Local Similarity   78.6%; Pred. No. 6.2e-62;
Matches 291; Conservative   0; Mismatches 73; Indels 6; Gaps 1;

```
Qy    24 GGTGGGAGTCTGGGGGAGGAGGCCCTGGCTCAAGCCTGGGGGGGTCCCTGAGACTCCTGTGCAGC 83
          |||||||||| || |||||| || | |  || ||||| ||| ||||||||||||| ||||||||
Db   489 GGTGGGAGTTCTGGGGGAGGCCTGGGTCCAGCCTCGGGAGGTCCCTGAGACTCTCCGTGTGCAGC 548

Qy    84 CTCTGGGATTCACCTTCAGTAGCTATAGCAATGGCACTGGGGTCCGCCAGGGTCCAGGGAAGGG 143
          |||||||||| ||||||| | || ||| |||| |||||||||||| |||||| |||||| ||||
Db   549 CTCTGGGATTCCCCTTCAGAAGCTTTGCTATTGCACTGGGGTCCCGCCAGGGCTCAGGGCAAGGG 608

Qy   144 GCTGGAGTGGGGTCTCATCCATTAGTAATAGTAATAACTTTACATATAATTACACGACGAGCCGT 203
          |||||||||||| |    |  ||||| || | || |  ||| || | |  |||  |  |    ||
Db   609 GCTGGAGTGGGTGGCAGTTATATCATATGAAGCACTAAATACTACCGCAGACTCCGT 668

Qy   204 GAAGGGCCGAGTTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAAATGAA 263
          ||||| |||| ||||||||| |||||| || ||| ||||| |||||| |||| ||||||||
Db   669 GAAGGGCCGATTCACCATCTCCAGAGACACTTCCAAGAACACGGTGTATCTAAGATACAGTAA 728

Qy   264 CAGCCTGAGAGCCGAGGACACACGGCTGTGTATTACTACTGCGCAGAGAGAGACGGCAGT 323
          ||||||||||| ||| |  ||| ||| || |||||||| ||  |||  ||| ||  || 
Db   729 CAGCCTGAGAACTGAGGACACGGCTGTCTATTACTGTGCCGAGGAT------CAGAGCCT 782
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```
Qy   324  TTTCCTCCGTTGGGGTTCGGAGCGACGGTATGGACGACGACGGTCAT 383
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   783  GTTTGGGTGACTATGACCACTACCGGTTTGGGACGTCTGGGGCAAAAGGGACCACGGTCAC 842

Qy   384  CGTCTCCCTCA 393
          |||||||||||
Db   843  CGTCTCCCTCA 852


RESULT 15
US-09-194-164-15/c
Sequence 15, Application US/09194164
GENERAL INFORMATION:
  APPLICANT: Dan, Michael D.
             Maiti, Pradip K.
             Kaplan, Howard A.
  TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT
                      SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
                      FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
                      DETECTION OF CANCERS
  NUMBER OF SEQUENCES: 18
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Morrison & Foerster
    STREET: 755 Page Mill Road
    CITY: Palo Alto
    STATE: CA
    COUNTRY: USA
    ZIP: 94304-1018
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/194,164
    FILING DATE: 09-Apr-1999
    CLASSIFICATION: <Unknown>
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/08/657,449
    FILING DATE: <Unknown>
  ATTORNEY/AGENT INFORMATION:
    NAME: Lehnhardt, Susan K.
    REGISTRATION NUMBER: 33,943
    REFERENCE/DOCKET NUMBER: 31608-20001.00
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (415) 813-5600
    TELEFAX: (415) 494-0792
    TELEX: 706141
INFORMATION FOR SEQ ID NO: 15:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 918 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-194-164-15

Query Match     58.8%;  Score 231.2;  DB 5;  Length 918;
Best Local Similarity   78.6%;  Pred. No. 6.2e-62;
Matches 291;  Conservative  0;  Mismatches  73;  Indels  6;  Gaps  1;

Qy    24  GGTGGAGTCTTGGGGGAGGCCGCGTGTCAAGCCTGGGGGGGGTCCCTGAGACTCTCCTGCAGC 83
          |||||||||| ||||| |||| ||| |||||||||||||||||||||||||||||||
Db   430  GGTGGAGTCGTGGGGGAGGCGGCTGGTCCCAGGCTCGAGACTCTCTCCGTGCAC 371

Qy    84  CTCTGGGATTCACCTTCACTAGCTGTATAGCATGCACTGGGTTCCCAGGGAAGG 143
          |||||||||| |||||||  ||||  | | |||||||||||| |||||||||||
Db   370  CTCTGGGATTCCCTTCAGAAGCTTTGCTACTGGGTCCGCCAGGCTCTAGGCAAGG 311

Qy   144  GGTGGAGTGGGGGTCTCATCCATTAGTAGTAATAATACTTTACATATACAGGCAGACGCAGT 203
          |||||||||| || |||||| ||||||| ||| | | | | ||||||||| ||||| |||
Db   310  GCTGGAGTGGGTGGCAGTTATATCATATATGGAAGCACTAAATACTACGCAGACTCCGT 251
```

```
Qy   204  GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
          |||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   250  GAAGGGCCGATTCACCATCTCCAGAGACAACTCACTGTATCTGCAAATGAA 191

Qy   264  CAGCCTGAGAGCCGAGGACACACGGCGTGTACTACTGTGCGAGAGATTCTAGATACAGTAA 323
          ||||||||||| |||||||||| |||||||  |||||||||||||||      ||||| ||
Db   190  CAGCCTGAGAACTGAGGACACGGCGTGTCTATTACTGTGCGAGAGAT------CAGAGCCT 137

Qy   324  TTTCCTCCGTTGGGTTTCGGAGCGACGACGGTATGGACGACTCTGGGGCCAAGGAGACCACGGTCAT 383
          |||  || | | | ||| || | | | ||||||||||| | |||||||| |||| ||||||||||
Db   136  GTTTGGGTGACTATGACCACTACCGGTTTGGGACGTCTGGGGCAAAGGGGACCACGGTCAC 77

Qy   384  CGTCTCCCTCA 393
          |||||||||||
Db   76   CGTCTCCCTCA 67


RESULT 16
US-10-031-722A-1
Sequence 1, Application US/10031722A
GENERAL INFORMATION:
  APPLICANT: Medarex, Inc.
  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HER2/NEU-
  FILE REFERENCE: MXI-160PC
  CURRENT APPLICATION NUMBER: US/10/031,722A
  CURRENT FILING DATE: 2000-07-25
  PRIOR APPLICATION NUMBER: USSN 60/146,313
  PRIOR FILING DATE: 1999-07-29
  PRIOR APPLICATION NUMBER: USSN 60/188,539
  PRIOR FILING DATE: 1999-03-10
  NUMBER OF SEQ ID NOS: 13
  SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
  LENGTH: 372
  TYPE: DNA
  ORGANISM: Homo sapiens
  FEATURE:
    NAME/KEY: CDS
    LOCATION: (1)..(372)
US-10-031-722A-1

Query Match     58.5%;  Score 230;  DB 6;  Length 372;
Best Local Similarity   78.6%;  Pred. No. 1.1e-61;
Matches 291;  Conservative  0;  Mismatches  70;  Indels  9;  Gaps  1;

Qy    24  GGTGGAGTCTTGGGGGAGGCCGCGTGTCAAGCCTGGGGGGGGTCCCTGAGACTCTCCTGTGCAGC 83
          |||||||||  ||||||||||  | | | |||||||||||||||
Db    12  GTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGGTCCC 71

Qy    84  CTCTGGATTCACCTTCAGTAGCTACTATAGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGG 143
          ||||||||||||||||| | ||||  |||  ||||||||||||||||||||||||||||||
Db    72  CTCTGGATTCACCTTTAGCAGCTATATGCACTGGGTCCGCCAGGCTCCAGGGAAGG 131

Qy   144  GCTGGAGTGGGTCTCATCCATTAGTAGTAATAATACTTTACATATACTACCAGACACGCAGT 203
          |||||||||||||||| |  | ||| ||| | | | | ||||| |||  |||| || ||
Db   132  GCTGGAGTGGGTCTCAGCTATCAGTGGTAGTTATACATACTACGCAGACTCCGA 191

Qy   204  GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
          |||||||||| ||||||||||||||||||  |||||||| | ||||||||||||||||||
Db   192  GAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAA 251

Qy   264  CAGCCTGAGAGCCGAGGACACACGGCGTGTTACTACTGTGCGAGAGATTCTAGATACAGTAA 323
          ||||||||||||||||||||| |||| ||| ||||||||||||||||   |||||| ||||
Db   252  CAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGATTTTGACTACTGGGGCCAA 309

Qy   324  TTTCCTCCGTTGGGTTCGGAGCGACGACGGTATGGACGACTCTGGGGCCAAGGGACCACGGT 383
          |||  |  | | | ||| || | | | ||||||||||| | |||||||||||| ||||||
Db   310  ------TCGGGGAGTTATTATACCCACTTTGACTACTGGGGCCAGGGAACCCTGGTCAC 362

Qy   384  CGTCTCCCTCA 393
          |||||||||||
Db   363  CGTCTCCCTCA 372
```

RESULT 17
US-09-194-164-18/c
; Sequence 18, Application US/09194164
; GENERAL INFORMATION:
;   APPLICANT: Dan, Michael D.
;   Maiti, Pradip K.
;   Kaplan, Howard A.
  TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT
          SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
          FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
          DETECTION OF CANCERS
  NUMBER OF SEQUENCES: 18
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Morrison & Foerster
    STREET: 755 Page Mill Road
    CITY: Palo Alto
    STATE: CA
    COUNTRY: USA
    ZIP: 94304-1018
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/194,164
    FILING DATE: 09-Apr-1999
    CLASSIFICATION: <Unknown>
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/08/657,449
    FILING DATE: <Unknown>
  ATTORNEY/AGENT INFORMATION:
    NAME: Lehnhardt, Susan K.
    REGISTRATION NUMBER: 33,943
    REFERENCE/DOCKET NUMBER: 31608-20001.00
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (415) 813-5600
    TELEFAX: (415) 494-0792
    TELEX: 706141
  INFORMATION FOR SEQ ID NO: 18:
    SEQUENCE CHARACTERISTICS:
    LENGTH: 867 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
    SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-09-194-164-18

  Query Match   58.4%; Score 229.6; DB 5; Length 867;
  Best Local Similarity   78.4%; Pred. No. 1.9e-61;
  Matches 290; Conservative   0; Mismatches 74; Indels   6; Gaps   1;

Qy   24 GGTGGAGTCTGGGGGAGGCGCCTCGGTCAACGTCCGGGGGGTCCCTGAGACTCTCCTGTGCCAGC 83
              ||||||||| ||| ||||||||||||||| ||||||||||| ||||||| |||||||||||||||
Db   430 GGTGGAGTCTGGGGGAGCCGTGGTCCACCTGGGGAGGGTCCCTGAGACTCTCCTGTGCCAGC 371

Qy   84 CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG 143
              |||||||||||||| |||| |||||| || |||||||||||||||||||||||| |||||
Db   370 CTCTGGATTCCCTTCAGAGAGCTTTGCTATGCACTGGGTTCCGCCAGGCTTCTAGGCAAGGG 311

Qy   144 GCTGGAGTGGGTCTCATCCATTAGTAATAGTAATAACTTACATATATACTACGGCGAGT 203
              ||||| ||| || ||| ||||| || |||||||||||| |||||| ||||||||||| |
Db   310 GCTGGAGTGGGTGGCAGTTATATCATTAGTGGAGCACTAAATACTACCAGGACTCCGT 251

Qy   204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
              ||||||||||||||||||| ||||||||||||||| |||||||||||| |||||||||||
Db   250 GAAGGGCCGATTCACCATCTCCAGAGACACTTCCAGAGACAACGTTGTATCTACAAATGAA 191

Qy   264 CAGCCTGAGAGACGCGACACACGGCCGTGTATTACTGTGCGAGAGATTCTAGATACAGTAA 323
              |||||||||||| | |||| ||||| |||| ||||||| | ||| | |||| || || |
Db   190 CAGCCTGAGAACTGAGGACACGGCGTGTCTATTACTGTGCGAGAGAT--------CAGAGCCT 137

RESULT 18
US-09-849-390-121
; Sequence 121, Application US/09849390
; GENERAL INFORMATION:
;   APPLICANT: Northwestern University
;   APPLICANT: ROWLEY, Anne
;   APPLICANT: BAKER, Susan
;   APPLICANT: SHULMAN, Stanford
  TITLE OF INVENTION: Methods and Compositions Related to Kawasaki Disease
    FILE REFERENCE: 0290-4601 (053662-5005-01)
  CURRENT APPLICATION NUMBER: US/09/849,390
    PRIOR FILING DATE: 2000-05-04
  CURRENT APPLICATION NUMBER: 2001-05-24
    PRIOR FILING DATE: 2000-05-04
  NUMBER OF SEQ ID NOS: 121
  SOFTWARE: Patentin version 3.0
  SEQ ID NO 121
    LENGTH: 360
    TYPE: DNA
    ORGANISM: Homo sapiens

US-09-849-390-121

  Query Match   57.8%; Score 227; DB 5; Length 360;
  Best Local Similarity   87.6%; Pred. No. 9.2e-61;
  Matches 248; Conservative   0; Mismatches 35; Indels   0; Gaps   0;

Qy   24 GGTGGAGTCTGGGGGAGGCGCCTCGGTCAACGTCCGGGGGGTCCCTGAGACTCTCCTGTGCCAGC 83
              ||||||||||| |||| ||| ||||| |||||||||| |||||||||||||||||||||||||||
Db   12 GGTGGAGTCTGGGGGGGCTTGGTGAAGCCTTCGGGGTCCCCGAGACTCTCCTGTGCCAGC 71

Qy   84 CTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG 143
              |||||||||||||||||| || || ||||||||||||| | |||||||||||||||| ||
Db   72 CTCTGGATTCACCTTCAGTGACTACTACATGAGTTGGGTTCGCCAGGCTCCAGGGAAGGG 131

Qy   144 GCTGGAGTGGGTCTCATCCATTAGTAATAGTAATAACTTACATATATACTACGGCGAGT 203
              ||||||||||| | || ||||||| || ||||| ||||||| |||||||||||||||
Db   132 ACTGGAGTGGGTTTCATATAGTTACTACATGAGTTATTACACAAAAGTAACGGCGAGT 191

Qy   204 GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAA 263
              ||||||||||||||||||| |||||||||||||||||||||||||| |||||||||||||
Db   192 GAAGGGCCGACTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTTCTGCAAATGAG 251

Qy   264 CAGCCTGAGAGACGCGACACACGGCCGTGTATTACTGTGCGAGA 306
              ||||||||| | || ||||| ||||||| ||||||||| |||||
Db   252 CAGCCTGAGAGCCGAGGACACGGCGTGTATTACTGTGCGAGA 294

RESULT 19
US-10-031-722A-5
; Sequence 5, Application US/10031722A
; GENERAL INFORMATION:
;   APPLICANT: Medarex, Inc.
  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HER2/NEU
    FILE REFERENCE: MXI-160PC
  CURRENT APPLICATION NUMBER: US/10/031,722A
    CURRENT FILING DATE: 2000-07-25
  PRIOR APPLICATION NUMBER: USSN 60/146,313
    PRIOR FILING DATE: 1999-07-29
  PRIOR APPLICATION NUMBER: USSN 60/188,539
    PRIOR FILING DATE: 1999-03-10
  NUMBER OF SEQ ID NOS: 13
  SOFTWARE: Patentin Ver. 2.0
  SEQ ID NO 5

The right column (continuation of RESULT 17):

Qy   324 TTTCCTCCGTTGGGTTCGGAGCGACGGACGTCTGGGGCCAAGGGACCACGGTCAT 383
              || | | | |||| |||||| || ||| | || ||||||||||||||||||
Db   136 GTTCGGGTGACTATGACCACTACTACGGTTTGGGTCGTCTGGGGCAAAGGGACCACGGTCAC 77

Qy   384 CGTCTCCTCA 393
              ||||||||||
Db   76 CGTCTCCTCA 67

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;    LENGTH: 366
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;      NAME/KEY: CDS
;      LOCATION: (1)..(366)
US-10-031-722a-5

Query Match             57.5%;   Score 226;  DB 6;  Length 366;
Best Local Similarity   78.4%;   Pred. No. 1.9e-60;
Matches  290;  Conservative   0;  Mismatches  65;  Indels  15;  Gaps  1;

Qy     24 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC  83
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     12 GGTGGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC  71

Qy     84 CTCTGGATTCACCTTCAGTAGCTATAGCCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG 143
          |||||||||||||||||||||||  || ||||||||||||||||||||||||||||  |||
Db     72 GTCTGGATTCACCTTCAGTAGCTATGACATACACTGGGTCCGCCAGGCTCCAGGGAAGGG  131

Qy    144 GCTGGAGTGGGGTCTCATCCATTAGTAATAGTAATAATTTACATATACTACGCAGACGCAGT 203
          ||||||||||                |  |  | | |  |  |  | || |||||||||||
Db    132 GCTGGAGTGGGGTGGCAGTAATAATGGTATGATGGCAGTAAATAAATACCATGCACGACTCCGT 191

Qy    204 GAAGGGCCGAGTTCAACCATCTCCAGAGACAACAGCCAAGAACTCACTGTATCGTCAAATGAA 263
          |||||||||||||||||  ||||||||||||||||||||||||||||| || | | || |
Db    192 GAAGGGCCGATTCACCATCTCCAGAGACAATTCAAGAACACGCTGTTACTGGTTTGGGGAG  251

Qy    264 CAGCCTGAGAGCCGAGCACACGGCTGTTGTTGCGAGATTCTTAGATACAGTAA  323
          |||||||||||||||||||||||||  |||||||||||||||||||||||||
Db    252 CAGTCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAAACTATGGTTTGGGGAG  311

Qy    324 TTTCCTCCGGTTGGGGTTCGGGAGACGTATGGACGTCTGGGGCCAAGGGACCACGGTCAT  383
          ||           |  | | || | | | ||
Db    312 TT---------ATTATAACTACTTTGACTTCTGGGGCGCCAGGGAACCCTGGTCAC  356

Qy    384 CGTCTCCTCA  393
          ||||||||||
Db    357 CGTCTCCTCA  366

Search completed: September 24, 2003, 05:54:52
Job time : 866 secs

RESULT 20
PCT-US03-25161-17
Sequence 17, Application PC/TUS03251161
GENERAL INFORMATION:
;     APPLICANT: Abgenix, Inc.
;     APPLICANT: Roskos, Lorin
;     APPLICANT: Foltz, Ian
;     APPLICANT: King, Chadwick
;     TITLE OF INVENTION: ANTIBODIES DIRECTED TO PARATHYROID
;     TITLE OF INVENTION: HORMONE (PTH) AND USES THEREOF
;     FILE REFERENCE: ABGENIX.092VPC
;     CURRENT APPLICATION NUMBER: PCT/US03/25161
;     CURRENT FILING DATE: 2003-08-08
;     NUMBER OF SEQ ID NOS: 97
;     SOFTWARE: FastSEQ for Windows Version 4.0
;
;    SEQ ID NO 17
;    LENGTH: 352
;    TYPE: DNA
;    ORGANISM: Homosapien
PCT-US03-25161-17

Query Match             57.5%;   Score 225.8;  DB 1;  Length 352;
Best Local Similarity   87.0%;   Pred. No. 2.2e-60;
Matches  248;  Conservative   0;  Mismatches  37;  Indels  0;  Gaps  0;

Qy     24 GGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGC  83
          ||||||||||||||||||||||||| ||| |||||||||||||||||||||||||||||
Db     12 GGTGGAGTCTGGGGGAGGCCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGC  71

Qy     84 CTCTGGATTCACCTTCAGTAGCTATAGCCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGG 143
          |||||||||||||||||| ||||||||  |  || |||||||||||||||| ||||| |||
Db     72 CTCTGGATTCACCTTCAGTAGCTATGGCATGGCCATGGGTCCGCCAGGCTCCAGGCAAGGG  131
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